

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 117161

TO: Nancy Vogel

Location: rem/2a65/2c70

Art Unit: 1636

Monday, March 29, 2004

Case Serial Number: 09/963285

From: Paul Schulwitz

Location: Biotech-Chem Library

REM-1A65

Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Vogel,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist STIC Biotech/Chem Library (571)272-2527



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Gaps

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PAT 10-APR-2003
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Mammalia, Eutheria; Primates, Catarrhini, Hominidae, Homo.
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         /organism='Unidentified'. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
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1 (bases 1 to 28)
Cochran,M.D. and Ounker,D.E.
Recombinant swinepox virus
Patent: US 6497882-A 265 24-DBC-2002;
                                                                                                                                                                                                                                                                                                                                              28 bp DN Sequence 265 from patent US 6497882.
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/db_xref="taxon:9606"
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Sequence 2 from Patent W00118039.
AX093873
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/organism="Homo sapiens"
                                                 1. .28
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/mol_type="genomic DNA"
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BARBARA J WINSLOW, WARK D COCHRAN
C12N15/09, A6IK39/12, A6IK39/125, A6IK39/15, A6IK39/215, A6IK39/23,
A6IK39/245,
A6IK48/00, A6IP43/00, C12N1/00//C07K14/705, C12N15/00 CC FIV
Keynstream primer
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1 (bases 1 to 28)
Winslow, B.J. and Cochran, M.D.
Recombinant virus expressing foreign DNA encoding felline CD80, felline CD86, felline CTRA-4 or felline interferon-gamma and uses stenent: JP 2002513581-A 75 14-MAY-2002;
SCHERING-PLOUGH LTD
OS Unidentified
NN JP 2002513581-A/75
PD 14-MAY-2002
PP 30-APR-1999 US 2000547248
PR 30-APR-1999 US 09/071711
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100.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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Sequence 84 from patent US 6221361.
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/mol_type="unassigned DNA"
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Location/Qualifiers
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BD273541.1 GI:33083309
JP 2002513581-A/75.
unidentified
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AR147023.1 GI:15110826
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COMMENT

STS 10-JUN-2003

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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales; Brasslcaceae, Arabidopsis.
                                                                                                                                                  BX322143 10-JUN-2003
Arabidopsis thaliana transposon insertion STS SM_3.35925, sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (31-MAR-2003) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 704, UK
AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gissociation transposon, M a mis-expression enhancer trap dissociation transposon, M a defective suppression enhancer trap transposon. 3 denotes a sequence derived from the 3'end of the transposon, BBSRC GARNet, ATIS project
On-line seed stock tequests: http://nasc.nott.ac.uk/ NASC stock
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/mol type="genomic DNA"
/variety="Columbia-0 NASC stock code N1092"
/db xref="taxon:3702"
/clone="AC006841"
/note="Derived from superpool 25.06 NASC code N41149"
                                                                                                                                                                                                                                                                                                                                                                                                                   Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Murphy, G., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M.
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Olivier, M. and Cox, D.R.
Unpublished, Olivier, M., Cox, D.R.
Unpublished (2000)
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Best Local Similarity 100.
Marches 12; Conservative
                                          102 GGAAAGTAAAA 113
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Unpublished
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SOURCE
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G55264/c
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                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; Pooideae, Bromeae, Bromeae, Bromeae, Bromes, Lo 150)

Paulsen, A., Meyer, S.E., Coleman, C.E. and Fairbanks, D.J.
Wicrosatellite markers for Bromus tectorum (cheatgrass)
Unpublished
Chases 1 to 150)
                                                                                                                                                         PLN 13-JUN-2000
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science, Brigham Young
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Patent: WO 0188188-A 468 22-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Submitted (21-Jan) Botany and Range Science, Brigh University, 401 WIDB, Provo, UT 84602, USA
Location/Qualifiers
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100.0%; Score 12; DB 6; Length 151;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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100.0%; Score 12; DB 8; Length 150;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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Sequence 468 from Patent WO0188188.
AX305717
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

March 25, 2004, 08:39:03 ; Search time 6718.14 Seconds (without alignments) 6361.316 Million cell updates/sec 1 ctgccattccaatccagcgc.....gagccgtctcggaagcagca 986 6940544 3470272 seqs, 21671516995 residues Total number of hits satisfying chosen parameters: US-09-963-285-1_COPY_1250_2235 986 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 GenEmbl:*
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Miura,N.
Direct Submission
Submitced (18-SEP-1996) N. Miura, Akita University School of
Medicine, Department of Biochemistry, 1-1-1 Hondo, Akita 010, JAPAN
Location/Qualifiers
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Homo sapiens chromosome 16 clone RP11-46309, complete sequence.
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DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission Submission Submitted (29-CCT-2002) DOE Joint Genome Institute, 2800 Mitchell Submitted (29-CCT-2002) DOE Joint Genome Institute, 2800 Mitchell On Oct 29, 2002 this sequence version replaced gi:13786306.

Draft Sequence Produced by DOE Joint Genome Institute
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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DOE Joint Genome Institute, Stanford Human Genome Center and
Alamos National Laboratory.
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Estimated Total Number of Errors is 0.2.
Location/Qualifiers
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US-09-328-352-713
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                                                                                                                                                                                                                                                         Sequence 1782, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
PAPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTEROCOCCUS FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 03796-03
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VERSION 3.1
                                                   Gaps
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0
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     Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 12; DB 4; Length 381; 100.0%; Pred. No. 1.1e+03;
                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Unmas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054FR2;
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 9538
IRNGTH: 535
  100.0%; Score 12; DB 3; I
100.0%; Pred. No. 1.1e+03;
                                                0; Mismatches
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; Patent No. 6475739
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0
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US-09-134-000C-1782
Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       513 GGAAAGTAAAA 524
                                                                                                                                                112 GGAAAGTAAAAA 101
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; ORGANISM: Homo sapiens
US-09-621-976-9538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 12, Conserv
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LENGTH: 381
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GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BLALELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
FILE REFRENCE: 62.013.CIP
CURRENT APPLICATION NUMBER: US/09/671,317
CURRENT APPLICATION NUMBER: US 09/536,178
PRIOR PILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: US/09/60126,269
PRIOR PILING DATE: US/09/126,269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: ATV I Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTS-09-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
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100.0%; Score 12; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0;
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APPLICANT: Paeper, Bryan
APPLICANT: Paeper, Bryan
APPLICANT: Stachling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: GENOMIC DELETIONS
FILE REPERENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
SEQ ID NO 7
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-671-317-429; Sequence 429, Application US/09671317; Patent No. 6528260
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; Sequence 713, Application US/09328352
Patent No. 6563958
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SEQ ID NO 713
                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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8
                                                                                                 APPLICANT: Oefner, Peter J.
APPLICANT: Underhill, Peter A.
APPLICANT: Underhill, Peter A.
TITLE OF INVENTION: Detection of DNA Heteroduplex Molecules
TITLE OF INVENTION: Detection of DNA Heteroduplex Molecules
TITLE OF INVENTION: Methods for Comparative Sequencing
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: RIXON, MARK W
APPLICANT: RADIAN, WARK W
APPLICANT: RADIAN, BONALD A
APPLICANT: SCHOLOM, UBFFREX
APPLICANT: SCHOLOM, UBFFREX
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSE: DUANE C ULMER
STREET: PFO. BOX 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 9; DB 1; Length 22; 100.0%; Pred. No. 2.8e+03; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) MOLECULE TYPE: DNA
) ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DYS234 REVERSE PRIMER
US-08-512-681-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE:
CLASSIFICATION: 435
TICNESIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: EVANS, SUSAN T.
REGISTRATION NUMBER: 36,443
REFERENCE/DOCKET NUMBER: 8600.
| INFORMATION FOR SEG ID NO: 19: SEQUENCE CHARACTERISTICS:
| LENGTH: 22 base pairs
| LENGTH: 22 base pairs
| TYPE: nucleic acid
| TYPE: nucleic acid
| TYPE: nucleic acid
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Patent No. 5993813
GENERAL INFORMATION
APPLICANT: (MEZES, PETER S
APPLICANT: GOUNTLE, BRIAN B
                                          Sequence 19, Application US/08512681
Patent No. 5795976
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
'Local 9; Conserva
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RESULT 11
US-08-512-681-19/c
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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APPLICANT: BERGERON, Michel G.
APPLICANT: BERGERON, Francois J.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 100.0%; Score 9; DB 2; Length 22; Best Local Similarity 100.0%; Pred. No. 2.8e+03; Matches 9; Conservative 0; Mismatches 0; Indels
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ZIP: 23.202-4497

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1:0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFTCATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BARKER, JGan C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,028
                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: ULAMEN, DUANE C
REGISTATION NUMBER: 34,941
REPERENCE/DOCKET NUMBER: C-37,075C
TELECOMUNICATION INFORMATION:
TELEPHONE: (S1) 636-8104
INFORMATION FOR SED ID NO: 35:
SECUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040,687
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 411 EAST WISCONSIN AVENUE
MILWAUKEE
WISCONSIN
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Patent No. 5994066
GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CLASSIFICATION:
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US-08-743-637B-240/C
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US-08-822-028-35
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CITY: MI
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March 25, 2004, 10:03:04; Search time 14.7262 Seconds (without alignments) 4297.861 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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17
1 tgtggaaggaataaata 17
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Gapop 10.0 , Gapext 1.0
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Maximum DB seg length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 9718, Ap	Sequence 107702,	Sequence 82796, A	Sequence 10003, A	Sequence 977, App	Sequence 1138, Ap	Sequence 64036, A	Sequence 17187, A	Sequence 22032, A	Sequence 242033,	Sequence 242034,	Sequence 141232,	Sequence 63676, A	Sequence 148185,
D	US-10-027-632-9718	US-10-424-599-107702	US-10-424-599-82796	US-09-764-891-10003	US-10-205-428-977	US-10-131-827-1138	US-10-424-599-64036	US-09-814-353-17187	US-10-424-599-22032	US-10-027-632-242033	US-10-027-632-242034	US-10-424-599-141232	US-10-424-599-63676	US-10-027-632-148185
DB	15	12	12	10	14	15	12	10	13	15	15	12	12	15
% Query Match Length DB	962	493	2523	21619	21619	20	359	386	493	589	589	909	616	919
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Result No.	H 0	1 M	4	Ŋ	9	7	co	σn	10	0 11	c 112	13	C 14	c 12

Sequence 37752, A	Sequence 43641, A	Sequence 256262,	Sequence 256263,	Sequence 256264,							Sequence 2121, Ap		8	급	w	Sequence 1367, Ap	(1)	689	Sequence 1369, Ap	Seguence 1368, Ap	_	Sequence 959, App	ì	e)	٠.	Sequence 1, Appli	Sequence 8323, Ap	Sequence 1, Appli	Sequence 234237,
US-10-424	US-10-424-599-4364	US-10-027-632-25626	US-10-027	US-10-027-632-25626	-			_		_	US-10-062-674-2121	US-09-963-285-5	US-10-221-613-351	US-10-198-846-13766	US-10-240-485-68	US-09-764-847-1367	US-10-092-154-1367	US-09-764-847-1368	US-09-764-847-1369	US-10-092-154-1368	US-10-092-154-13	6	US-09-747-810-1	US-10-003-806-	US-10-003-806	US-10-043-715-1	US-10-424-599-8		US-10-027-632-234237
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90.6	90.6	90.6	90.6	90.6	9.06	9.06	9.06	90.6	90.6	90.6	90.6	90.6	9.06	9.06	90.6	90.6	90.6	90.6	90.6	90.6	90.6	90.6	90.6	90.6	90.6	90.6	88.2	88.2	
15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15	15	15
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ALIGNMENTS

·. Length 962; Indels Query Match
100.0%; Score 17; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; 9718, Application US/10027632 lon No. US20030204075A9 ---

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Gaps

US-09-963-285-1

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Sequence 82796, Application US/10424599
Publication No. US2004031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy 10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 82796
LENGTH: 2523
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Sequence 10003, Application US/09764891

Publication No. US20030077808A1

Publication No. US20030077808A1

ARPLICANT: ROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC006

CURRENT PILION DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 10231

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10003

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SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10003
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100.0%; Pred. No. 6.5e+02;
cive 0; Mismatches 0;
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US-10-424-599-82796
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2 GTGGAAGGAATAATA 17
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Sequence 107702, Application US/10424599
Fublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rose Thomas J
APPLICANT: Cao Yongweil
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 107702
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NAME/KEY: unsure
(1): (493)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                          Patent No. US20020090707A1
GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: Krock, Katarina
APPLICANT: Krock, Katarina
APPLICANT: Rondahl, Lenna
APPLICANT: Rondahl, Lenna
APPLICANT: Rondahl, Lenna
APPLICANT: RONDAHL, Wyeth
TITLE OF INVENTION: PROMOTER SEQUENCES
FILE REPERENCE: 13425-042001
CURRENT FILING DATE: 2001-09-26
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RRICK FILING DATE: 2000-11-09
FRICK APPLICATION NUMBER: SE 0003435-5
FRICK APPLICATION NUMBER: SE 0003435-5
FRICK APPLICATION NUMBER: SE 0003435-5
FRICK FILING DATE: 2000-09-26
FRICK FILING DATE: FASESEQ for Windows Version 4.0
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   727 IGIGGAAGGAAIAAIA 743
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; LOCATION: (2235)...(3737)
US-09-963-285-1
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SEQ ID NO 1 LENGTH: 6458

TYPE: DNA

d à

Sequence 977, Application US/10205428

Publication No. US20030108907A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

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Query Match 94.1%; Score 16; DB 12; Length 493; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 16; Conservative 0; Mismatches 0; Indels

; FEATURE: ; OTHER INFORMATION: Clone ID: PAT_MRT3847_68271C.1 US-10-424-599-107702

TYPE: DNA

US-10-205-428-977/c

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

March 25, 2004, 08:39:03; Search time 81.7624 Seconds (without alignments) 6361.316 Million cell updates/sec

US-09-963-285-1_COPY_1692_1703 Title: Perfect score:

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

r.	144897 Sequence 34	AR147023 Sequence	AR267926 Sequence	AX093873 Sequence	AF227460 Bromus te AY305717 Semience	BX322143 Arabidops	G55264 SHGC-100532	Axsusses seguence BD044918 Seguence	AJ578474 Brassica	AL009426 H.sapiens	AF184852 Arabidops AU046405 Rattus no	G74846 STS6-204 Sm	U1831/ Bacillus su AJ431205 Nicotiana	AF288758 Cryptobia	BX322133 Arabidops AY019564 Orvza sat	BX322076 Arabidops	BX322104 Arabidops	Y15668 Homo sapien	AJ594039 Arabidops	AUSYGIOS ATADIGODS G23240 human STS W	AY036343 HIV-1 180	Z51097 H.sapiens (AJ588365 Arabidops	AX910794 Sequence	BD046327 Sequence AB043926 Homo sapi	AB043909 Homo sapi	AB043910 Homo sapi AB043911 Homo sapi	AB043932 Homo sapi	AB043939 Homo sapi	AB043942 Homo sapi Rh204302 5'EST and	AB073287 Macaca fu	AL807135 Arabidops X17266 Zebrafish h			linear PAT 07-0CT-1997			and Clouthier, S.C.		
e e							G55264	BD04491	BNA578474		AF18485 AU0464	G74846										HS189XB										11 AL807135 5 BRHOX61	ALIGNMENTS	٠	19 bp DNA patent US 5635617.	10		W., Collinson, S. Karen.	TOTAL COMPTENDING	-A 34 03-JUN-1997;
Length D						4 1-4	(1)	NN	10	(3.6	N N	010	N C	1011	010	1 (7)	010	4 (4	C) C	N N	101	m r	n m	(M)	ריז נייז	m	יי) ניי	ניה ני	(7)		וייי ו	330			34 from p	GI:24696		ified. es 1 to 19) .L., Kay,W.W.	la Ta	
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PAT 10-APR-2003
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Score 12; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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            /organism='Unidentified'
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—Inseres86 production of interferon—g(a)
Patent: WO 0118039-A 2 15-MAR-2001;
GLAXO GROUP LIMITED (GB)
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Cochran,M.D. and Junker,D.E.
Recombinant swinepox virus
Patent: US 6497882-A 265 24-DEC-2002;
Location/Qualifiers
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Sequence 265 from patent US 6497882.

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Best Local Similarity 100.um
Trahes 12; Conservative
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Matches 12, Conservative
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SOURCE
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01-May-1999 US 09/017111
BARBARA J WINSLOW MARK D COCHRAN
CIZNIS/09,A61K39/12,A61K39/125,A61K39/15,A61K39/23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BD273541 linear PAT 17-JUL-Recombinant virus expressing foreign DNA encoding feline CD80, feline CD86, feline CTLA-4 or feline interferon-gamma and uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 28)
Winslow, B.J. and Cochran, M.D.
Recombinant virus expressing foreign DNA encoding feline CD80,
feline CD86, feline CTLA-4 or feline interferon-gamma and uses
Patent: JP 2002531381-A 75 14-MAY-2002;
SCHERING-PLOUGH LID
                                                                                                                               Gaps
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A61K48/00,A61P43/00,C12N7/00//C07K14/705,C12N15/00 CC
downstream primer
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0
                                                                                              100.0%; Score 12; DB 6; Length 19; 100.0%; Pred. No. 5.9e+04; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 28)
Cochran, M.D. and Junker, D.E.
Recombinant swinepox virus
Patent: US 6221361-A 84 24-APR-2001;
Location/Qualifiers
               1. .19
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                             AR147023 28 bp 1
Sequence 84 from patent US 6221361.
AR147023. GI:15110826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unknown"
/mol_type="unassigned DNA"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
JP 2002513581-A/75
14-MAY-2002
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BD273541.1 GI:33083309
JP 2002513581-A/75.
unidentified
                                                                                              Query Match
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                              Unclassified.
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AR147023/c
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BD273541/c
LOCUS
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ORGANISM
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Submitted (31-MAR-2003) Clarke J.H., John Innes Centre, Colney Submitted (31-MAR-2003) Clarke J.H., John Innes Centre, Colney Jane, Norwich, NR4 7UJ, UK and denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, MR a defective suppressor minator transposon. 3 denotes a sequence derived from the 3'end of the transposon BRSRC GARNet, ATIS project Continue seed stock requests: http://nasc.nott.ac.uk/ NASC stock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear STS 30-MAR-2000
                                                                                                                                                BX322143 19-JUN-2003
Arabidopsis thallana transposon insertion STS SM_3.35925, sequence
                                                                                                                                                                                                                                                           STS; STS, sequence tagged site.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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G55264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/waltety="Columbia-0 NASC stock code N1092"
/db xref="taxon:3702"
/clone="Act06841"
/note="Derived from superpool 25.06 NASC code N41149"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Murphy, G., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 191)
                                   102 GGAAAGTAAAA 113
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1 GGAAAGTAAAA 12
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                                                                                                                                                                                           tagged site.
BX322143
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Best Local Similarity
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clarke, J.H.
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G55264/c
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                                                                                                                                                   linear PLN 13-JUN-2000
                                                                                                                                                                                                                                                                                   Bromus tectorum

Bromus tectorum

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooldeae, Bromeae, Bromus.

Posideae, Bromeae, Bromus.

Paulsen, A., Meyer, S.E., Coleman, C.E. and Fairbanks, D.J.

Microsatellite markers for Bromus tectorum (cheatgrass)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Paulsen, A., Meyer, S.E., Coleman, C.E. and Fairbanks, D.J.
Paulsen, A., Meyer, S.E., Coleman, C.E. and Fairbanks, D.J.
Direct Submission
Submitted (21-JAN-2000) Botany and Range Science, Brigham Young University, 401 WIDB, Provo, UT 84602, USA
Location/Qualifiers
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Method: WO 0189188-A 468 22-NOV-2001;
School Juridical Person Nihon University (JP)
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                                                                                                                                       Ar.27.460 150 bp DNA linear
Bromus tectorum clone 21 microsatellite sequence.
AF227460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Bromus tectorum"
/mol_type="genomic DNA"
/db_xref="taxon:29667"
/clone="21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AX305717
Sequence 468 from Patent W00188188.
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="microsatellite"
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                                                                                                                                                                                                                     AF227460.1 GI:8489262
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  1 GGAAAGTAAAA 12
                                        12 GGAAAGTAAAA 23
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AF227460/c
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Gaps

COMMENT

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Divaryota; Eucheria; Craniata; Vertebrata; Buteleostomi; Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

El (Dases 1 to 207)

E dwards, J.B.D.M., Duclair, E. and Jordan, J.Y.

Sequence tag and encoded human protein

Datent: JP 2001269182-A 21164 02-0CT-2001;

GENSET

OS Homo sapiens (human)

PN JP 2001269182-A/21164

PD 02-0CT-2001

PP 24-FEB-2000 JP 2000118773

PR 26-FEB-1999 US 60/122487

PI JEAN BAPUTIST DUMAS MILNE EDWARDS, BIMERIC DUCLAIR, JEAN YVES

PI JORDAN

PC CI2NIS/09, C07K14/435, C07K16/18, C12NI/15, C12NI/19, C12NI/21, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 bp DNA linear PLN 25-OCT-2003 protein, IGS and partial pebC gene for PSII 43 kDa AJ578474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GOFF15/40
GOFF15/40
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IGS; intergenic spacer; psbC gene; PSII 43 kDa protein; transfer RNA-Ser (UGA); tRNA-Ser (UGA) gene.
RNA-Ser (UGA); tRNA-Ser (UGA) gene.
Brassica napus (rape)
Brassica napus (rape)
Brassica napus (rape)
Brixaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                     Query Match 100.0%; Score 12; DB 6; Length 207; Best Local Similarity 100.0%; Pred. No. 4.1e+04; Matches 12; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 4.1e+04;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                           Sequence tag and encoded human protein.
/mol_type="unassigned DNA"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                        ED044918.1 GI:22586660
JP 2001269182-A/21164.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.
Matches 12; Conservative
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PC C12P2:
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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94 degrees C for 30 seconds
60 degrees C for 30 seconds
72 degrees C for 23 seconds
30
Perkin Elmer 9700
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        Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5801
Fax: (650) 320-5801
Email: olivierSebgc.stanford.edu
Primer A: TCACTTAACTTTGCGAACCCATT
Primer B: CTAGTGTTTGCTTCCCTTCCCT
FCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 25248 06-SEP-2000; Genset (FR)
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100.0%; Score 12; DB 11; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels (
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each 1 uM
each 200 uM
0.07 units/ul
5 ul
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Organism="Homo sapiens"
Organism="Homo sapiens"
Moltype="genomic DNA"
/db_xref="taxon:9606"
/map="14"
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Total Vol:
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/organism="Homo sapiens"
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50 mM
10 mM
8.3
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19. .145
19. .41
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Annealing:
Polymerization:
PCR Cycles:
Thermal Cycler:
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Homo sapiens
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dNTPs:
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primer_bind
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FEATURES

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Gaps 0

AX909385 LOCUS

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FEATURES

'clone="SC1pE10B10"

/sex="female"

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                                                                                                Direct Submission
Submitted (25-UTL-2003) Day A., School of Biological Sciences,
University of Manchester, 3.614 Stopford Building, Oxford Road, M13
9PT, UNITED KINGDOM
Location/Qualifiers
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(Dases I to 210)

Gregory, S., Kettleborough, R., Langford, C., Ross, M.T. and Hunt, S.E. Direct Submission

Submitted (03-DEC-1997) E-mail contact; humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marker stSG29044 (Primer A : CTTCATTCTAACTCCTGTCCCA, Primer B : TCATAAAGCCAACTGATTGAA, amplimer size : 143 bp) was mapped to chromosome 1 using Radiation Hybrid panel Genebridge 4 (GB4).
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Zubko,M.K., Zubko,E.I., van Zuilen,K., Meyer,P. and Day,A. Stable plastid transformation of Petunia plastids Unpublished
2 (bases 1 to 209)
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                                                                                                                                                                                                                                                                                                                                                                          /function="photosynthetic protein"
/codon start=1
/transI table=11
                                                                                                                                                                                                                   /organism="Brassica napus"
/organelle="plastid:chloroplast"
/wol_type="genomic DNA"
/cultivar="nare"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
/product="PSII 43 kDa protein"
/proteinid="CAB18106.1"
/db xref="GI:37992040"
/translation="MTPLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19. .193
/note="intergenic spacer, IGS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement [194, 209)
/gene="tRNA-Ser (UGA)"
complement [194, .209)
/gene="tRNA-Ser (UGA)"
/product="tRNA-Ser"
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/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                               /db_xref="taxon:3708"
1. .18
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STS; single read.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                         gene="psbC"
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AL009426
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...rhes 12; Conservative
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Actius norvegicus, OTSUKA clone, 0147B, microsatellite sequence, and other sequence, 0147B, microsatellite sequence, other sequence.
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Manoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
1 (bases 1 to 229)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Stickema, W.J. and Pereira, A.

Direct Submission
Submitted (13-SBP-1999) Molecular Biology, CPRO-DLO, P.O. Box 16, Mageningen 6700AA, The Netherlands
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spellman, E., Metz, P.L., van Arkel, G., te Lintel Hekkert, B., Stiekema, M.J. and Pereira, A. A. two-component enhancer-inhibitor transposon mutagenesis system for functional analysis of the Arabidopsis genome Plant Cell 11 (10), 1853-1866 (1999)
                                                                                                                                                         Gaps
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                                                                                                        100.0%; Score 12; DB 11; Length 210; 100.0%; Pred. No. 4.1e+04; ative 0; Mismatches 0; Indels C
/tissue type="BBV lymphoblastoid cell line"
/clone lib="SC1pE"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 12; DB 8; Length 229; 100.0%; Pred. No. 4e+04; ative 0; Mismatches 0; Indels
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
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Rattus norvegicus
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KEYWORDS
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Watanabe, T.K., Hishigaki, H., Okuno, S., Mizoguchi, A., Oga, K.,
Tsuji, A., Ono, T., Yamasaki, Y., Kanemoto, N., Takahashi, E., Irie, Y.,
Takagi, Y. and Tanigami, A.
The large-scale mapping of rat microsatellite markers

L Unpublished

E (Dasses I to 247)

S Watanabe, T.K.

Direct Submission

L Submitted (II-DEC-1998) Takeshi K Watanabe, Otsuka GEN Research

Institute, Otsuka Pharmaceutical Co., Ltd, 465-10, Kagasuno,
Kawauchi-cho, Tokushima, Tokushima 771-0192, Japan

(E-mail:watanabe@otsuka.gr.jp, Tel:+81-886-65-2888,
Fax:+81-886-37-1035)

Location/Qualifiers

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/srzafia-"Brown Norway"
/db xref="taxon:10116"
/clone="01478"
/csloue="1 type="hepatocyte"
/tissue type="liver"
/nore="01478F=5'-TCACATCCACCATCCTCAAAT-3',
01478R=5'-ACAACTTATTACCTGCCCAGACC-3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 12; DB 11; Length 247; Best Local Similarity 100.0%; Pred. No. 4e+04; Matches 12; Conservative 0; Mismatches 0; Indels
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Search completed: March 25, 2004, 12:49:42 Job time : 85.7624 secs

98 GGAAAGTAAAA 109

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Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Patent No. 5,85259 Sequence 14, Appl Sequence 13, Appl Sequence 632, Appl

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US-08-811-682-14
US-08-857-076-43
US-08-857-076-43
US-09-221-0178-632
US-08-35-517-115-186
US-08-955-1715-186
US-08-955-547-9
US-08-315-547-9
US-09-946-239-7
            US-10-079-616-5
US-09-873-404-1
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Best Local Similarity 100.
Matches 12; Conservative
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 US-08-233-788A-34
 RESULT 1
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Sequence 26, Appl
Sequence 80, Appl
Sequence 1782, Appl
Sequence 1782, Appl
Sequence 7, Appl
Sequence 7, Appli
Sequence 429, Appl
                                                                                 March 25, 2004, 09:55:14; Search time 2.36035 Seconds (without alignments) 2821.370 Million cell updates/sec
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2, Appli
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/cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-686-986C-84
US-08-303-040-80
US-09-303-040-80
US-09-134-000C-1782
US-09-611-976-9538
US-09-911-686-7
US-09-912-686-7
US-09-1317-429
US-09-134-000C-701
US-09-134-000C-701
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US-09-134-000C-701
US-09-134-000C-701
US-09-134-000C-701
US-09-1312-203
US-08-59-171-17
US-09-641-638-525
US-08-59-171-17
US-09-641-638-525
US-08-59-171-17
US-09-641-70-17
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US-09-620-312D-404
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Maximum Match 100%
Listing first 45 summaries
                                                             nucleic search, using sw model
                                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB
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                                                                                                                                                                                                               APPLICANT: Doran, James L.
APPLICANT: Xay, William W.
APPLICANT: Collinson, Xaren S.
APPLICANT: Clinison, Sharon C.
TITLE OF INVENTION: WETHOUS AND COMPOSITIONS FOR DET
TITLE OF INVENTION: OF SALMONELLA
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/233,788A
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua REGISTRENCE/DOCKET NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 35,570
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Machington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-233-788A-34/c
; Sequence 34, Application US/08233788A
Patent No. 56356.7
; GENDERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: Other nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPERATING SYSTEM: PC-DOS/KS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRINT APPLICATION DATE:
PTLING DATE: 07-Jun-1995
CLASSIFICATION: CUNKNOWN>
ATTORNEY ARGENT INFORMATION:
NAWE: Salkeld, Pamela G.
                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 12; DB 3; Length 28; 100.0%; Pred. No. 1.1e+03; tive 0; Mismatches 0; Indels
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Sequence 265, Application US/08472679H

Sequence 265, Application US/08472679H

GENERAL INFORMATION:

APPLICANT: Cochran, Mark D.

JUNKER, David E.

TITLE OF INVENTION: Recombinant Swinepox Virus

NUMBER OF SEQUENCES: 267

CORRESPONDENCE ADDRESSE:

STREET: 2000 Galloping Hill Road
                                                                                                           APPLICANT: Junker, David E.
TILE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML US/08/686,968C
CURRENT APPLICATION NUMBER: US/08/686,968C
CURRENT FILING DATE: 1996-07-25
SOFTWARE PATENTING DATE: 231
SOFTWARE PATENTIN Ver. 2.1
SEQ ID NO 84
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION UNBER: 38,607
TELECOMMUNICATION INFORMATION:
TELEPAX: (908) 298-2135
TELEPAX: (908) 298-3388
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
                            1, Application US/08686968C
5221364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
ULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
                                                                                              Cochran, Mark D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGAAAGTAAAA 12
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HYPOTHETICAL: NO
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                 US-08-686-968C-84/c
                                         ; Sequence
RESULT 2
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APPLICANT: Winelow, Barbara J.

APPLICANT: Cochran, Mark D.

TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
TITLE OF INVENTION: Recline CD80, Feline CD86, Feline CTLA-4 or
TITLE OF INVENTION: Feline Interferon-gama And Uses Thereof
FILE REFERENCE: 54957-B

CURRENT APPLICATION NUMBER: US/09/303,040

CURRENT FILING DATE: 1999-04-30

EARLIER APPLICATION NUMBER: 60/083,870

EARLIER APPLICATION NUMBER: 60/083,870

EARLIER APPLICATION NUMBER: 00/083,870

EARLIER APPLICATION NUMBER: 00/083,870

EARLIER APPLICATION NUMBER: 00/083,870

EARLIER PLING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 82

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 80
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GENERAL INCORDANT:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION UNMER: US/09/385,982
CURRENT TILING DATE: 1999-08-30
EAALIER PILING DATE: 1999-06-08
EAALIER PILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER PILING DATE: 1999-01-27
EARLIER PILING DATE: 1999-01-27
SEALIER PILING DATE: 1999-01-27
SEALIER PILING DATE: 1999-01-1
NUMBER OF SEQ ID NOS: 544-08-31
NUMBER OF SEQ ID NOS: 544-08-31
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 361
                                                                                                       100.0%; Score 12; DB 4; Length 28; 100.0%; Pred. No. 1.18+03; Live 0; Mismatches 0; Indels
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ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 265: US-08-472-679H-265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA; TYPE: DNA; OKGANISM: FIV PPR downstream primer US-09-303-040-80
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10S-08-385-982-26/c
1 Sequence 26, Application US/09385982
1 Patent No. 6262334
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Sequence 80, Application US/09303040

Patent No. 6555671

GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(361)
COTHER INFORMATION: n = A,T,C or G
                                                                                                                                    Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                    1 GGAAAGTAAAA 12
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GENERAL INFORMATION:
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US-09-134-000C-1782/C
US-09-134-000C-1782/C
Sequence 1782, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US 60/05134,000C
CURRENT BILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR RIPER DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN version 3.1
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100.0%; Score 12; DB 4; Length 381;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels
                Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 535;
                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9558, Application US/09621976; Sequence 9558, Application US/09621976; Patent No. 6639063; GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S. T. TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335; SOFTWARE: Patent.pm
SEQ ID NO 9538
LENGTH: 535
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100.0%; Pred. No. 1.1e+03;
:ive 0; Mismatches 0;
            Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0;
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US-09-318-686-7
'Sequence 7, Application US/09918686
'Patent No. 6475739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecalis
US-09-134-000C-1782
                                                                                                                                112 GGAAGTAAAA 101
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                          1 GGAAAGTAAAA 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-9538
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US-09-621-976-9538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1782
LENGTH: 381
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Sequence 429, Application US/09671317
Sequence 429, Application US/09671317
Patent No. 6528260
GENERAL INFORMATION:
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
TITLE OF INVENTION BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
TITLE OF INVENTION NUMBER: US/09/671,317
CURRENT APPLICATION NUMBER: US 09/536,178
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,269
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 1999-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: GETOT.
TITLE OF INVENTION: ACCEPTED AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TILE REPERENCE: GTOS9-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 6778
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APPLICANT: Brunkow, Mary
APPLICANT: Proll, Sean
APPLICANT: Pacper, Bryan
APPLICANT: Stachling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: 04003.515
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 713, Application IIS/09328352
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 602
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-671-317-429
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TOPOLOGY: line
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US-09-114-000C-701/C

US-09-114-000C-701/C

Patent No. 6617156

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT ON:

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTERCOCCUS FAECALLS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SEQ ID NO 701

LENGTH: 732

LENGTH: 732
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                                                                                                                                                                                                  NAME/KEY: allele
LOCATION: 364
COTHER INFORMATION: 12-622-325 : polymorphic base C or T
NAME/KEY: misc. binding
LOCATION: 344.363
COTHER INFORMATION: 12-622-325.misl, potential
NAME/KEY: misc. binding
LOCATION: 355.384
COTHER INFORMATION: 12-622-325.misl, potential complement
NAME/KEY: primer bind
LOCATION: 355.384
COTHER INFORMATION: upstream amplification primer
NAME/KEY: primer_bind
LOCATION: 351.569
COTHER INFORMATION: upstream amplification primer
NAME/KEY: primer_bind
LOCATION: 351.569
COTHER INFORMATION: downstream amplification primer, complement
NAME/KEY: misc_binding
LOCATION: 352.366
COTHER INFORMATION: 12-622-325 potential probe
NAME/KEY: misc_feature
LOCATION: 333,865,688
COTHER INFORMATION: n=a, g, c or t
US-09-671-317-429
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PRIOR APPLICATION NUMBER: US 60/131,961
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 977
SEQ ID NO 429
LENGTH: 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              668 GGAAAGTAAAAA 679
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Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
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RESULT 12 US-09-023-655-875

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Gaps

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NAME/KEY: misc_binding

LOCATION: 502..521

OTHER INFORMATION: 10-298-158.mis2, potential complement

NAME/KEY: primer_bind

LOCATION: 348..365

OTHER INFORMATION: upstream amplification primer

NAME/KEY: primer_bind

LOCATION: 770..789

OTHER INFORMATION: downstream amplification primer

NAME/KEY: misc_binding

LOCATION: 489..513

OTHER INFORMATION: 10-298-158 potential probe

US-09-641-638-525
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APPLICANT: Wang, Dunrul
APPLICANT: Wang, Dunrul
APPLICANT: Wang, Lininglast
APPLICANT: John Tillinglast
APPLICANT: Drmanac, Radoje T.
ITILE OF INVENTION: Dolypeptides
FILE OF INVENTION: Dolypeptides
FILE REPERENCE: 784CIP2B
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR PILING DATE: 2000-04-25
PRIOR PRILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARR: PEL Genes Version 1.0
SEQ ID NO 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 12; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0;
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100.0%; Score 12; DB 4; L
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0;
                                        LOCATION: 481.7500
OTHER INFORMATION: 10-298-158.misl, potential
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US-09-620-312D-203
; Sequence 203, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tang Y. Tom
APPLICANT: Tang Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Xao, Qing A.
APPLICANT: Xao, Aidong J.
APPLICANT: Yang, Yorghong
APPLICANT: Yang, Yorghong
APPLICANT: And, Yang, Jian-Rui
APPLICANT: Zhou, Ping
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ma, Yunging
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; LOCATION: (93)..(1082)
US-09-620-312D-203
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patent No. 6432646

GENERAL INPORMATION

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Chunakov, IIya

APPLICANT: Chunakov, IIya

APPLICANT: Chen, Annick

TITLE OF INVENTION: BLALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

TITLE OF INVENTION: GENES 105/09/641, 638

CURRENT FILING DATE: 2000-08-16

PRIOR FILING DATE: 2000-02-11

PRIOR FILING DATE: 1999-05-07

PRIOR FILING DATE: 1999-05-07

PRIOR FILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 1304

SSOFTWARE: PATENT PATENT IN STATES IN 
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LOCATION: 501

COTHER INFORMATION: 10-298-122 : polymorphic base C or T
NAME/KEY: misc_binding

LOCATION: 481.500

COTHER INFORMATION: 10-298-122.misl, potential

NAME/KEY: misc_binding

LOCATION: 502.521

COTHER INFORMATION: 10-298-122.mis2, potential complement

NAME/KEY: primer_bind

LOCATION: 384.401

COTHER INFORMATION: upstream amplification primer

NAME/KEY: primer_bind

LOCATION: 806.432

COTHER INFORMATION: 000-038

LOCATION: 806.432

COTHER INFORMATION: 10-298-122 potential probe

USCATION: 489.513

COTHER INFORMATION: 10-298-122 potential probe
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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels (
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LOCATION: 501
OTHER INFORMATION: 10-298-158 : polymorphic base A or G
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR PILING DATE: 1999-03-23
PRIOR PEDLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
LENGTH: 1001
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                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo Sapiens
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Search completed: March 25, 2004, 15:34:19 Job time : 4.36035 secs

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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PETY LENGTH DB ID 10.0 3289 9 HSMPH1 6.8 168656 9 AC009108 6.9 168656 9 AC009108 8.0 10 2000 0 MAMFHEAD1 8.0 1 10 2000 0 MAMFHEAD1 8.1 17445 2 AC009108 8.1 17445 2 AC009108 8.2 172457 2 BX664728 8.2 172457 2 BX664728 8.3 1 11305 8 AC009109 8.4 2000 0 AC009108 8.5 1 11305 8 AC009109 8.6 1 10 2000 0 AC009109 8.7 2 10 2000 0 AC009109 8.8 1 11305 8 AC009109 8.9 1 10 2000 0 AC009109 8.0 28474 2 AC009109 8.0 28477 2 AC009109 8.0 2849900 8.0 28477 2 AC009109 8.0 284			ď				
1 986 100.0 3289 9 HSNFH1	esul No	Score	Query Match		DB	Ω	escription
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RESULT 1 HSMFH1 LOCUS	DEFINITION ACCESSION VERSION	KEYWORDS	ORGANISM	REFERENCE AUTHORS TITLE

PRI 14-MAY-1997

ALIGNMENTS

Mura,N., Iida,K., Kakinuma,H., Yang,K.L. and Sugiyama,T. Isolation of the mouse (MPH-1) and human (FKHL 14) mesenchyme fork head-1 genes reveals conservation of their gene and protein a; Euteleostomi; ae; Homo.

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AC009108 168656 bp DNA linear PRI 29-OCT-2002
Homo sapiens chromosome 16 clone RP11-46309, complete sequence.
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Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
National Laboratory
www-shgo.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
1. .168656
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
AACTITICCCAAICCCTAAAAGGGACTIGGCCTCTTTTTCTGGGCTCAGCGGGGGAGCCG, 751
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DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
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DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Submitted (29-OCT-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Wahnut Creek, CA 94598, USA
On Oct 29, 2002 this sequence version replaced gi:13786306.

Draft Sequence Produced by DOE Joint Genome Institute
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Miura, N.
Direct Submission
Submitted (18-SEP-1996) N. Miura, Akita University School of Medicine, Department of Blochemistry, 1-1-1 Hondo, Akita 010, Location/Qualifiers
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                                                                                                                                                           Score 954; DB 9; I
Pred. No. 4.7e-163;
0; Mismatches 5;
/mol_type="genomic DNA"
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/clone="RP11-46309"
                                                                                                                                                              96.8%;
ilarity 99.3%;
Conservative
                                                                                                                                                              Query Match
Best Local Similarity
Matches 979; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Park
                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 178416)
Cordes, M. and Haglund, K.
The sequence of Mus musculus BAC clone RP24-323X23
Unpublished (2001)
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Mus musculus BAC clone RP24-323K23 from chromosome 8, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-AUG-2003) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA (E. Chases 1 to 178416) Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Sequencing Center, 4444 Forest 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://genome.wustl.edu.
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: M_BB0323K23
76525 GCCGGCGAGCCGTCTCGGAAGCAGCA 76500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
3 (bases 1 to 178416)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing of Mus musculus
                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (17-JUL-2002)
Parkway, St. Louis, MO 6
4 (bases 1 to 178416)
                                                                                                                                                                                                     GI:33457241
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5 (bases 1 to 178416)
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Direct Submission
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Submitted (17-JUL
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AC127554.4
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This sequence was finished as follows unless otherwise noted:

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see

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39272 TTTGCTCTGAACCCATTACAACTAGGCCCCGATAATTAAGAAATCTAATTCGCCTCT 39331
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                                                                                        75547. 135866

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47365. 47488

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47067. 47550

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47067. 47580

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                                                                                                                                                                                                                                                                                                                                                                             1423. .52857
note="CpG_island (%GC=66.5, o/e=0.72, #CpGs=121)"
3367. .53484
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30.3%; Score 298.6; DB 10; Length
Best Local Similarity 64.7%; Pred. No. 4.9e-44;
Matches 595; Conservative 0; Mismatches 269; Indels
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/xpc_family="B4"
47952. .48067
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60886. .61042
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                          SOURCE INFORMATION:
The RFCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                                                        NEICHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone is
overlapped by AC124170.
                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                          /mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="8"
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i. 26022
family="MER1_type"
                                                                                                                                                                                                                                              clone="RP24-323K23"
                                                                                                                                                                                                                                                           clone_lib="RPCI-24"
791. _1839
                                                                                                                                              Location/Qualifiers
1. .178416
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9. .20683
family="Alu"
4. .20799
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8974. 19317
rpt family="MalR"
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rpt_family="MalR"
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|2192, 32221
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32923. .33036
/rpt_family="Alu"
33141. .33245
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973. .400c
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                                                                                                                                                                                                                                                                          1. .20013
family="B2"
8. .20538
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30809. and
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rpt_family="B4"
846. .3972
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9. .30963
family="Alu"
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rpt_family="B4"
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1950. | 20010
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8

55; Gaps

Length 178416;

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Direct Submission
Submitted (18-SEP-1996) N. Miura, Akita University School of
Medicine, Department of Biochemistry, 1-1-1 Hondo, Akita 010, JAPAN
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DRFPFYRENKQGMQNSIRHNLSLNECFVKVPRDDKKPGKGSYWTLDPDSYNMFENGSF
LRRRRRFKKKDVPKDKEERAHLKEPPSTTAKGAPTGTPVADGPKEAEKKVVVKSEAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PALEVITKVETLSPEGALOASPESASSTPASSPDGSLEEHHAARDGLEGFSVETIM
LRTSPEGGIDASPAARAGGVVPPLALEYAAAPPANTVOPCAGGLEAAGSAGYQCSMRA
MALYUGABRPAHVCVPPALIDEALSDHPSGFGSPLGALNIAAGGEGALGASGHHHQHHG
HLHPQAPPPAQPPPAPQPATQATGWYLNHGGDLSHLPGHTFATQQOTFPNVEMFNS
HRLGLDNSSLGESQVSNASCQLPYRATPSLYRHAAPYSYDCTKY"
                                                                                                                                                                                                                                                                                                                                                                                                                     /protein id="CAA69399.1"

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/db_xref="G26A:0G150E980"

/db_xref="SWISS-PROT:0G1850"

/translation="MQARYSVSDPNALGVVPYLSEQNYYRAAGSYGGMASPMGVYSGH
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and
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/product="mesenchyme_fork head-1 protein"
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 gene
genes reveals conservation of their
                                                                                                                                                                                                     1. .6021
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129"
/db_xref="taxon:10090"
                           Genomics 41 (3), 489-492 (1997)
97312712
                                                                                                                                                                                 Location/Qualifiers
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/gene="MFH-1"
2070. .3554
/gene="MFH-1"
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2070. .3554
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Miura,N.
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3932 TCATCCATTAATAATAATAAAAAAAAATCTCCAGGCTCTTTCCTACTTACAAGGTCTTG 39391
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Isolation of the mouse (MFH-1) and human (FKHL 14) mesenchyme fork
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Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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mesenchyme fork head-1 protein; MFH-1 gene.
Mus musculus (house mouse)
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M.musculus MFH-1 gene.
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VERSION
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AUTHORS
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 159805;
                                                                                                                                                                                                                                            12 89708: contig of 89708 bp in length

1709 89808: gap of 100 bp

1809 112141: contig of 22333 bp in length

1742 112241: gap of 100 bp

1742 135060: contig of 22819 bp in length

1751 159805: contig of 24645 bp in length.

1751 Location/Qualifiers
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/note="assembly_fragment:00365.0"
135161. 159805-
/note="assembly_fragment:01064"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Danio rerio"
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon.7955"
/clone="DKBY-4017"
/clone="DKBY-4017"
/clone="lib="DanioKey"
/ note="assembly fragment:01665
fragment_chain:1"
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fragment_chalu..
89809. .112141
/note="assembly_fragment:00508
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51.8%; Pred. No. 7.3e-06;
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Matches 225;
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PM2A12B/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (23-SBP-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-helpssanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 24, 2003 this sequence version replaced gi:32959697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopierygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
[ Lo 159805 ]
                                                                                                                                                                                                                               1685 GCTCTCCGGACCCTAGCTCGCTGACGCTGCGGGCTGCAGTTCTCCTGGCGGGGCCCCGAG
                                                                                                                                                                                                                                                                                                                       AGCCTCCTGCGCCCCTCGCGCGCGCGCGGGGTCCACCTTGGTCCCCAGGCCGCGGGG
                                                                                                                                                                                                                                                                                                                                                                                       ------CTGGTGTCGCTCCA
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                                                                                                                             1625 TIGAAACTITTCCCAATCCCTAAAAGGGACTTTGCTTCTTTTCCGGGCTCGGCGAA
                                                                                                                                                                                             GCCGCT - CGGACCCCGGCGCGCGCTGACCTTCGCTGCCGATTCGCTGG-GGGCTTGGAG
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Consensus quality: 157884 bases at least Q40
Consensus quality: 15816 bases at least Q30
Consensus quality: 158516 bases at least Q20
Insert size: 159505; sum-of-contigs
Insert size: 16481; 0.9% error; agarose-fp
coverage: 10.03x in Q20 bases; sum-of-contigs Quality
coverage: 9.49x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BX546449.3 GI:35209399
HTG, HTGS_PHASE1, HTGS_PRAFT, HTGS_FULLTOP.
Danio rerio (zebrafish)
Danio rerio
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BX546449
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
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Submitted (05-NOV-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries:
Zish.help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 7, 2003 this sequence version replaced gi:37805598.
                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, etinopersygii, Neopeerygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Danio.

( Pases 1 to 172457)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      583 GGGGGCTTGGAGAGCCTCCTGCGCCCCTCCTCGCGCGGGCCGAGGGTCCACCTTGGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemistry: Dye-terminator, 100% of reads
Consensus quality: 171280 bases at least Q40
Consensus quality: 171415 bases at least Q30
Consensus quality: 171619 bases at least Q20
Insert size: 172357; sum-of-contigs
Insert size: 177300; 44% error; agarose-fp
Quality coverage: 10.42x in Q20 bases; sum-of-contigs Quality
coverage: 10.22x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.2%; Score 80.6; DB 2; Length 172457; llarity 50.8%; Pred. No. 0.00019; Conservative 0; Mismatches 209; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 110971: contig of 110971 bp in length 110972 111077: gap of 100 bp 11072 172457: contig of 61386 bp in length. Location/Qualifiers
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish).
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="assembly_fragment:01040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment:00009
fragment_chain:1
                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4; version 4.5
                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/db xref="taxon,7955"
/clone="CH211-108M10"
/clone lib="CHORI-211"
1. 110971
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clone end:T7
vector side:left"
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      PM2A12B 869 bp DNA linear STS 29-MAY-2003
Penicillium marneffei STS, clone pm2a12.b, sequence tagged site.
                                                                                                                                                         Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes;
Gurotiales, Trichocomaceae, mitosporic Trichocomaceae, Penicillium.
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                                                                                                                                                                                                                                                                                                                                               (bases 1 to 869)
Danchin, A. and Pascal, G.
Direct Submission
Submitted (08-WAR-2002) Danchin A., HKU-Pasteur Research Centre,
Dexter HC Man Building 8, Sassoon Road, Pokfulam, Hong Kong
Location/Qualifiers
                                                                                                                                                                                                                 Yuen,K.Y., Pascal,G., Wong,S.S., Glaser,P., Woo,P.C., Kunst,F.,
Cai,J.J., Cheung,B.Y., Medique,C. and Danchin,A.
Exploring the Penicillium marneffei genome
Arch. Microbiol. 179 (5), 339-353 (2003)
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48.9%; Pred. No. 3.7e-05;
tive 0; Mismatches 226; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Penicillium marneffei"
/mol_type="genomic DNA"
/db_xref="taxon:37727"
/clone="pm2a12.b"
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Penicillium marneffei
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Homo sapiens chromosome 15 clone CTD-3026N10 map 15, LOW-PASS SECTIONS SAPELING.
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103 TGAAGACGGAGTCGCCGCGGAGGCCGGGGGGGGGGGGTCTTAGAGGCGAAGGGGAATTCCTGC 362
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 51753)

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                         627 YMSTGMYGAYSSYKSMSWTSKASYMGKOATCTMYTSMKGSTRRSKMGRWSGMSRMYMRWWK
                                                                                                                                                                                                                                                                507 YCWYYYYGMYMKCSYMMRYGYCKACKKCCYAMCWKAAYSGMMMYWYRKYSKWMRMSTKYM
                                                                                                                                                                                                                                                                                                                                            CGGGAGGGGGGGGCGTGGGAAGGTAAAACTCGCTTTCAGCAAGAAGACTTTTGAAA
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                                                                                                                                                                                                                                        CITITICCCAATCCCTAAAAGGGACTTGGCCTCTTTTTCTGGGCTCAGCGGGGCAGCCGCT
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Homo sapiens chromosome 15, clone CTD-3026N10
Unpublished
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Homo sapiens (human)
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Patent: WO 03000898-A 5263 03-JAN-2003;
Syngenta Participations AG (CH)
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                                                             761
                                                                                                                                                                                                                                                                                                    Oryza sativa
kukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideee, Oryzeae, Oryza.
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                                                             GTCCTGGAGCCAGCGAGCGGGGCCGGCGCTGCGCTTGCCCG-GGGCGCGCCCTCCAG
                                                                                                 762 GATGCCGATCCGCCCGGTCCGCTGAAAGCGCCCCCCCCTGCTCGGCCCCGAGCGACGA
                                                                                                                                                                                                                     CCGCGCACCCTCGCCCCCGGAGGCTGCCAGGAGCCGGGCCGCCCCTCCCCCTCC
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    .2000
    /organism="Oryza sativa"
    /mol_type="unassigned DNA"
    /db_xref="taxon:4530"

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Barren, B., Nusbaun, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaun, C., Lander, B., Chompel, Y., Collymore, A., Camarata, J., Chang, J., Collymore, A., Cooke, P., DeArellano, K., Diaz, J.S., Dodge, S., Paro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardhan, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, T., Johnson, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Mecdonald, P., Major, J., Mathews, C., Murphy, T., Naylor, J., Nguyen, C., Micol, R., Mathews, C., Norman, C., Norman, C., Norman, C., Norman, J., Phunkhang, P., Plerrs, N., Raymond, C., Retta, R., Seeman, S., Severy, P., Seman, J., Schauer, S., Schubback, R., Seeman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodorer, S., Schubback, R., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

L. Submitted (17-Jul-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 17, 2002 this sequence varsion replaced gi:21426260.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker:html
                           Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kartas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Landers, T., Landers, T., Maclean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Mencus, L., Mihova, T., Menga, V., McKernan, K., Meldrim, J., Mencus, L., Mihova, T., Menga, V., Murbhy, T., Naylor, J., O'Donnell, P., O'Neill, D., Ollver, J., Peterson, K., Phunkhang, P., Paterre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Ries, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Sender, S., Severti, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., You, Wilson, B., Mu, X., Wyman, D., Ye, W.J., Young, G., Dbhaission
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   Goyette, M., Graham, L.
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Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* Will be sequenced to completion. In the event that
* the record is updated, the accession number will
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   Galagan, J., Gardyna, S., Ginde, S., Gord, S.,
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COMMENT

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Pred. No. 0.00023;
0; Mismatches 310; Indels 0;
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Estren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Boguslavkiy, L., Boukgaler, B., Brown, A., Burket, G., Collins, S., Campopiano, A., Castle, A., Chospel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fatzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, N., Klein, J., Lakocque, K., Landers, T., Landers, T., Lahoczky, J., Levine, K., Landers, T., Lahoczky, J., Levine, K., Lieu, G., Locke, K., Macdonald, P., Marquis, N., McDwan, P., McDwan, P., McGwan, R., McDwan, P., McGwan, P., Marada, C., Mlenga, V., Marda, C., Mledin, J., Maylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Neil, D., O'Neil, D., O'Neil, D., O'Livar, T.M., Olivar, J., Spencer, B., Spencer, B., Stanger-Thomann, N., Schauer, S., Severy, P., Spencer, B., Stanger-Thomann, N., Schauer, S., Severy, P., Spencer, B., Tragilio, J., Tragilico, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Voung, G., Zalmoun, J., Zimmer, A. and Zody, M.

Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker:html
HTG 30-MAR-2000
LOW-PASS
                                                                                                                                                                                                                                                                                Eukaryord, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

[ (Dases 1 to 75144)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 3, clone RP11-336E13
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* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
    75144 bp DNA linear chromosome 3 clone RP11-336E13 map 3,
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4: contig of 762 bp in length

5: gap of 100 bp

6: contig of 762 bp in length

6: gap of 100 bp

7: contig of 759 bp in length

7: contig of 759 bp in length
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Pred. No. 0.00024;
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DRWDYVLMAVGSLGACAHGASYPVFFIFFGKLINIIĞLAYLFPTTVSGRVAKYSLDFV
YLGIVILFSSWTEVACWMHTGERQAARORQAYLRSMLDQDIAVFDTEASTGEVINAIT
SDLIVVQDALSEKVONFMHYISRFLAGFALGFSQWOISLIVTLAIVPLTALAGGIYAY
VIIGLMARVRKSYVRAGEIAEEVIGNOFFVGERKAVRTYREALLRTYKGKRG
LAKGGLGSMHSVLFSFABALLIWFTSVVVHRNISNGSESFTTMLNVYLAGLSGQAAB
NISTFLRARTAAXPIFQMIERNTVNKASSKAGRTLPSVDGHIQFRDVFRYFSRPDVV
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Place Croix du Sud, 2/20, 1348,
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RQQIGLVNQEPALFATSIRENILYGKGDASMDEINHAAKLSEAITFINHLPDRYETQV
GERGIQLSGGQKQRIAISRAILKNPSILLLDEATSALDAESEKSVQEALDRVMVGRTT
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SEOSASLSRENESKYSRELSKYSORESTREMOSVSKYGTVETKHEDGGHKSKPVSMKK
LYSKIRPDRFFGVSGTVSARVASORMELFALGVTOALVSYYMGWETTKREVKTAVLF
CCGAVLTVVPHALEHLSFGIMGERLTLRVRERMFAALLRNEIGWFDDTSHTSSMLSSR
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/db_xref="SPTREMBL:Q8GU75"
/translation="MSSPVHGVQEHRQSGGGEKKAEQGEKEAAAKVEKVFFLKLFSFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AJ53561
AJ53561. GI:27368850
MDR-like ABC transporter; mdr11 gene.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                               326 GCACCCTCGCCCCGGAGGCTGCCAGGAGCCGGCCGCCCCTCCCGCTCCCTCTCTC
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/mol=stref="taxon:39947"
1. .11305
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/product="MDR-like ABC transporter"
/protein_id="CADS9583.1"
/db_xref="GI:27388851"
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Submitted (27-NOV-2002) Ducos E.,
Unite de Biochimie Physiologique,
BELGIUM
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/gene="mdr11"
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Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Penicillium.
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Danchin, A. and Pascal, G.
Direct Submission
Submitted (08-MAR-2002) Danchin A., HKU-Pasteur Research Centre, Dexter HC Man Building 8, Sassoon Road, Pokfulam, Hong Kong Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunst, F.,
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Cai,J.J., Cheung,E.Y., Medigue,C. and Danchin,A.
Exploring the Penicillium marneffel genome
Arch. Microbiol. 179 (5), 339-353 (2003)
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"Mol type="genomic DNA"
|db_xref="texon:37727"
|clore="pm/f8.g"
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8.1%; Score 79.6; DB 11;
Best Local Similarity 50.7%; Pred. No. 0.00015;
Matches 229; Conservative 0; Mismatches 219;
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ALGSS189
ALGSS189.1 GI:19336534
STS.
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85434 bp DNA linear HTG 04-JUN-2000 HOMO sapiens chromosome 15 clone CTD-2242M2 map 15q15, LOW-PASS ACOGEC10
                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases I to 85434)

1 (Dases I to 85434)

Bloom, S., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A., Nesbitt, R., Shaffer, T. and Hood, L.

2 (Dases I to 85434)

2 (Dases I to 85434)

Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Jumes, R., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., James, R., Kaur, A., Madan, A., Owen, M.P., Ratcliffe, A., Shaffer, T.
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Submitted (25-APR-2000) Multimegabase Sequencing Center, University
of Washington, PO BOX 357730, Seattle, WA 98195, USA
On Jun 4, 2000 this sequence version replaced gi:7644476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: UWMSC
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: learowen@systemsbiology.org
Contact: Summary Statisfics
Sequencing vector: pUG18; 108752
Chemistry: Dye-terminator 13ig Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This record contains 96 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
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Homo sapiens (human)
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                                                                                                                                                                   VERSION
KEYWORDS
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JOURNAL
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Query Match 8.1%; Score 79.6; DB 8; Length 11305; Best Local Similarity 55.4%; Pred. No. 0.00021; Matches 211; Conservative 0; Mismatches 164; Indels 6;

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Gaps ý

	unknown length of 809 bin 10 unknown length of 816 bp in 1 unknown length of 817 bp in 1 unknown length of 811 bp in 1 unknown length of 813 bp in 1 unknown length of 813 bp in 1 unknown length of 814 bp in 1 unknown length of 806 bp in 1 unknown length of 819 bp in 1	
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t be assumed that this clone completion. In the event that, the accession number will nig of 817 bp in length p of unknown length p of unknown length p of unknown length nig of 784 bp in length nig of 784 bp in length nig of 784 bp in length nig of 786 bp in length nig of 786 bp in length nig of 796 bp in length nig of 796 bp in length p of unknown length nig of 798 bp in length p of unknown length	contig of 794 bp in length contig of 08 05 bp in length contig of 192 bp in length contig of 164 bp in length contig of 180 bp in length contig of 803 bp in length contig of 803 bp in length contig of 805 bp in length contig of 805 bp in length contig of 787 bp in length contig of 787 bp in length contig of 789 bp in length contig of 788 bp in length contig of 788 bp in length contig of 788 bp in length contig of 789 bp in length contig of 189 bp in length contig of 189 bp in length contig of 803 bp in length	unkno of 81 unkno of 81
However, it should will be sequenced is update be preserved. 1 175: 918 1075: 1176: 1971: 1975: 2072 2855: 2256 2955: 2556 3851: 3752		8238 28337: 8338 29155: 9156 29255: 9256 30067:

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Submitted (16-JAN-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA On Jan-16, 2003 this sequence version replaced gi:26665814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-primer ET; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 223474 bases at least Q40
Consensus quality: 223474 bases at least Q20
Consensus quality: 223020 bases at least Q20
Insert size: 220000; agarose-fp
Insert size: 22504; sum-of-contigs
Quality coverage: 11.88 in Q20 bases; sum-of-contigs
                                                                                                                                         Center: Washington University Genome Sequencing Center
Center code: WUGSC
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107777. .224777
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Mus musculus chromosome UNK clone RP24-444115, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       565
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Mus musculus (blosse mouse)

Mus musculus (blosse mouse)

Mus musculus (blosse mouse)

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

(bases 1 to 22477)

MCPherson, J. D. and Waterston, R. H.

The sequence of Mus musculus clone

Onpublished of mus musculus clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 85434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.0%; Score 79.2; DB 2; Length 85 Best Local Similarity 48.7%; Pred. No. 0.00032; Matches 219; Conservative 0; Mismatches 229; Indels
         64420: contig of 803 bp in length 64520: gap of unknown length 65428: contig of 808 bp in length 65428: gap of unknown length 66234: contig of 806 bp in length 67118: contig of 784 bp in length 67118: gap of unknown length 6708: gap of unknown length 68008: contig of 796 bp in length 68008: contig of 795 bp in length 68008: contig of 793 bp in length 68001: contig of 793 bp in length
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McPherson, J.D. and Waterston, R.H.
Direct Submission
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2. (bases 1 to 93821)

Birren B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Bouchaller, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Dowin, M., Doyle, M., Fenestor, J., Ferreira, P., Firzhdgh, W., Forrest, C., Gageb, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Hackord, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, P., Macdorald, P., Marquis, N., McEwan, P., McCurk, A., McKernan, K., McMenters, R., Meldrim, J., Meneus, L., McCurk, A., McKernan, K., Flers, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Pierre, N., Eisani, C., Pallon, C., Liu, G., Looke, K., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Flers, R., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Storamanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Lirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., J., Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Conjul 13, 2000 this sequence version replaced gi:6705503.

All repeats were identified using RepeatMasker:
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Homo sapiens clone RP11-165K4, LOW-PASS SEQUENCE SAMPLING.
ACC21596
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 93821)
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Length 224777;
      Score 79; DB 2; Length 224
Pred. No. 0.00038;
0; Mismatches 176; Indels
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al Similarity 52.4%;
197; Conservative
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Homo sapiens (human)
Homo sapiens
      Query Match
Best Local Similarity
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* NOTE: This record contains 93 individual
sequencing reads that have not been assembled into
contigor. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
                                                                                                                        Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: project Information
Center project name: 15/87
Center clone name: 165_K_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : cont. 2

2: contig of 902 bp in length

2: gap of 100 bp

58: contig of 946 bp in length

68: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8: gap of 100 bp
6: contig of 908 bp in length
5: gap of 100 bp
1: contig of 904 bp in length
1: gap of 100 bp
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contig of 738 bp in length
gap of 100 bp
contig of 923 bp in length
gap of 100 bp
contig of 939 bp in length
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of 889 bp in length
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contig of 944 bp in length
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contig of 939 bp in length
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of 887 bp in
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contig of 929
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57: gap of 911 bp in length
50: contig of 893 bp in length
50: gap of 100 bp
22: contig of 882 bp in length
23: gap of 100 bp
24: contig of 800 bp in length
35: gap of 100 bp
36: contig of 886 bp in length
37: gap of 100 bp
                                                                                                                                       gap of 100 bp contrig of 924 bp in length gap of 100 bp contrig of 835 bp in length gap of 100 bp contrig of 835 bp in length gap of 100 bp contrig of 835 bp in length gap of 100 bp contrig of 922 bp in length gap of 100 bp contrig of 932 bp in length gap of 100 bp contrig of 932 bp in length gap of 100 bp contrig of 932 bp in length gap of 100 bp contrig of 939 bp in length gap of 100 bp contrig of 939 bp in length gap of 100 bp contrig of 939 bp in length gap of 100 bp contrig of 939 bp in length gap of 100 bp contrig of 935 bp in length gap of 100 bp contrig of 935 bp in length gap of 100 bp contrig of 935 bp in length gap of 100 bp contrig of 935 bp in length gap of 100 bp contrig of 935 bp in length gap of 100 bp contrig of 935 bp in length gap of 100 bp contrig of 935 bp in length gap of 100 bp contrig of 935 bp in length gap of 100 bp contrig of 935 bp in length gap of 100 bp contrig of 935 bp in length gap of 100 bp contrig of 935 bp in length gap of 100 bp contrig of 935 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 bp in length gap of 100 bp contrig of 930 b
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Pred. No. 0.00038;
0; Mismatches 234; Indels 2;
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contig of 918 bp in length

gap of 100 bp

contig of 907 bp in length

gap of 100 bp

contig of 83 bp in length

contig of 827 bp in length

contig of 927 bp in length

gap of 100 bp

contig of 912 bp in length

gap of 100 bp

contig of 910 bp in length

gap of 100 bp

contig of 901 bp in length

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Search completed: March 25, 2004, 12:49:38 Job time : 6724.14 secs

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CITY: Los Angeles
STATE: Californía
COUNTRY: U.S.A.
                           US-08-758-306-137/c
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Sequence 1139, App
Sequence 1109, Ap
Sequence 5500, Ap
Sequence 5500, Ap
Sequence 5501, Ap
Sequence 2391, Ap
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                                                                                         March 25, 2004, 09:55:14; Search time 1.77026 Seconds (without alignments) 2821.370 Million cell updates/sec
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Sequence 2392,
Sequence 137, A
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-758-306-139
US-08-758-306-11109
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US-08-758-306-111109
US-08-78-104-5501
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US-09-38-268-34
                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                             682709 segs, 277475446 residues
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                                                                                                                                                             US-09-963-285-1_COPY_223_231
                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               - nucleic search, using sw model
                                                                                                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued Patents NA:*
                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                              1 acaaatgtt 9
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Match Length
                                                                                                                                                                                score:
                                                                                                                                                                                                                             Scoring table:
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                                                               OM nucleic
                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                              Title:
Perfect
                                                                                                Run on:
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No.
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Length 17;
               APPLICANT: MCSA'SGEN, James A.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES
TITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
NUMBER OF SEQUENCES: 1379
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 9; DB 1; Li 100.0%; Pred. No. 2.8e+03;
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; Patent No. 5807743
; GENERAL INFOWATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: MCSWiggen, James A.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOD AND REAGENT FOR TH
TITLE OF INVENTION: TREATMENT OF DISBASES
TITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
NUMBER OF ENCURNICES: 1379
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                    STREET: SUITE #30.0 STREET: SUITE #30.0 CITY: Los Angeles STATE: Los Angeles STATE: California COUNTRY: U.S.A. CALIfornia COUNTRY: U.S.A. CALIFORNIA STATE: SONTI-2066 COMPUTER READMBLE FORM: MEDIUM TYPE: Storage COMPUTER: IEM COMPATIBLE COMPUTER: IEM COMPATIBLE CONTRARE: FastSeq Version 1.5 CURRENT APPLICATION DATA: APPLICATION: S14 PRIOR APPLICATION: 514 PRIOR APPLICATION: 514 PRIOR APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                              E: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERNICE/DOCKET NUMBER: 212,
TELECOMUTNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (7-3510
INFORMATION FOR SEQ ID NO: 1109:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 9; Conservative
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-758-306-1111/c
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Length 17;
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                                             0; Indels
                                                                                                                                                                                                                                                    Sequence 139, Application US/08758306
Fatent No. 5807743
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
ITLE OF INVENTION: METHOD AND REAGENT FOR THE
ITILE OF INVENTION: METHOD AND SEASON
ITILE OF INVENTION: INTERLEUKIN-2 RECEPTOR
ITILE OF INVENTION: GAMMA-CHAIN EXPRESSION
ITILE OF SEQUENCES: 1379
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon.
CHERCEL LYON & LYON.
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CHERCEL LYON & LYON.
CHERCEL LYON & LYON.
DB 1; Le
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. 2.8e+03;
                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER RADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compediable
COMPUTER: IBM Compediable
COMPUTER: FARESON THE P.C. DOS 5.0
SOFTWARE: FARESON THE P.C. DOS 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION S14
PRIOR APPLICATION S14
PRIOR APPLICATION MUMBER: 212/132
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REFERENCS/DOCKET NUMBER: 212/132
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 67-3510
INFORMATION POR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
Query Match 100.0%; Score 9; Best Local Similarity 100.0%; Pred. No. Matches 9; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 9; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: 634 West Fifth Street CITY: Los Angeles COUNTRY: U.S.A. ZIPE: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 9; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                              1 ACAAATGTT 9
                                                                                                                                         12 ACABATGTT 4
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US-08-758-306-139/c
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US-08-758-306-139
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STREET: CITY: LC STATE: C

RESULT 3
US-08-758-306-1109/c
Sequence 1109, Application US/08758306
Patent No. 5807743
GENERAL INFORMATION:

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Gaps
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Fatent No. 6346398

BAPELICANT: Pavco, Pamela

APPLICANT: Pavco, Pamela

APPLICANT: Browding, James

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Bscobedo, Jaimes

TITLE OF INVENTION: RETHORN OF DISEASES OR

TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL

TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL

TITLE OF INVENTION: GROWTH FACTOR

NUMBER OF SEQUENCES: 8502

CORRESPONDENCE ADDRESS:

ADDRESSESE: Lyon & IT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0;
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CITY: Los Angeles
COUNTY: U.S.A.
ZIP: 90071-2066
COMPUTER: READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 600764
MEDIUM TYPE: 15% COMPUTER: 100 NOT 100 N
                 PALLOR AFFILATION TUMBER: 60/005,974
PILING DATE: October 26, 1995
ATTORNEY/AGRET INCRNATION:
NAME: WALBULG, RICHARD 32,327
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INCORMATION:
TELEFAN: (213) 999-1600
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 5500: SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5501:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
       PRIOR APPLICATION DATA:
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US-08-584-040-5500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5500, Application US/08584040

Patent No. 6346338
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: TREATMENT OF DISEASES OF
TITLE OF INVENTION: TREATMENT OF DISEASES OF
TITLE OF INVENTION: OF VACULAR ENDOTHELIAL
TITLE OF INVENTION: OF VACULAR ENDOTHELIAL
TITLE OF INVENTION: GROWHY FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 90701-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8torage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
                                                                                                                                                              COMPOTER: IBM Compatible
COMPOTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,22/13
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 1111:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACAAATGIT 9
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 ACAAATGTT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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US-08-584-040-5500/c
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Sequence 137, Application US/09780175
Patent No. 6440738
GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Susan M. Freier
APPLICANT: Jacquelline Wyatte
TITLE OF INVENTION: ANTIESSEE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION
FILLE REFERENCE: RTS-0164
CURRENT APPLICATION NUMBER: US/09/780,175
CURRENT FILLING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 154
EBNGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Robert McKay
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Jacquelline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION
FILE REFERENCE: RTS-0164
CURRENT APPLICATION NUMBER: US/09/780,175
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 154
ELECTION OF SEQ ID NOS: 154
ELECTION OF SEQ ID NOS: 154
ELECTION OF SEQ ID NOS: 154
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                                                                                                                                                     Length 17;
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100.0%; Score 9, DB 4; Lo
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 9; DB 4; Le
ilarity 100.0%; Pred. No. 2.8e+03;
Conservative 0; Mismatches 0;
                                                                                                                                                  100.0%; Score 9; DB 4; I 100.0%; Pred. No. 2.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Antisense Oligonucleotide US-09-780-175-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Antisense Oligonucleotide US-09-780-175-138
                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 138, Application US/09780175 Patent No. 6440738 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 ACAAATGTT 12
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Best Local Similarity
Local 9; Conserv?
                     ; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2392
                                                                                                                                                                                                                                                                                                                                                                                                         US-09-780-175-137/c
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US-09-780-175-138/c
SEQ ID NO 2392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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APPLICANT: Pavco, Pam
APPLICANT: Backingen, Jim
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT APPLICATION NUMBER: US 60/05,974
PRIOR APPLICATION NUMBER: US 60/05,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: McSwiggen, Jim
APPLICANT: StinchComb, Dan
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US 09/371, 772B
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                           0, Indels
                                                                                                                                                                     Query Match
100.0%; Score 9; DB 4; L.
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
US-09-371-772B-2391/c
US-09-371-772B-2391, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-371-772B-2392/c

Sequence 2392, Application US/09371772B

PREENT NO 6566127

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 9; Conservative
                        LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                            11 ACAAATGTT 3
                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2391
                                                                                                 7 TOPOLOGY: ]
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RESULT 13
US-08-443-637B-240/C
Sequence 240, Application US/08743637B
Sequence 240, Application US/08743637B
Sequence 240, Application US/08743637B
Sequence 240, Application US/08743637B
Sequence 240, Application US/087481
APPLICANT: PICARD, Francois J.
APPLICANT: PICARD, Francois J.
APPLICANT: ROY, Paul H.
APPLICANT: WAND WAND AND SESSER SERVING SESSER FROM CLINICAL SPECIMENS
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS
CORRESPONDENCE ADDRESS:
ADDRESSEE: 4018-ADDRESS:
CONTRESPONDENCE ADDRESS:
ADDRESSEE: 4018-ADDRESS:
CONTRESPONDENCE ADDRESS:
ADDRESSEE: 4018-ADDRESS:
ADDRESSEE: 4018-ADDRESS:
ADDRESSEE: 4018-ADDRESS:
ADDRESSEE: 4018-ADDRESS:
ADDRESSEE: 4018-ADDRESSEE: ADDRESSEE: ADDRES
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Le
2.8e+03;
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Best Local Similarity 100.0%; Pred. No. 2.8
Matches 9; Conservative 0; Mismatches
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586,90012
                                                                                                                                                                                                                                                                                                            APPLICALL...

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUGNE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TENGTH: 122 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR PELLCATION DATA:
APPLICATION NUMBER: US 08/040,687
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                                                                      GENERAL INFORMATION:
Patent No. 579596
GENERAL INFORMATION:
PAPLICANT: Obfier, Peter J.
APPLICANT: Underhill, Peter A.
TITLE OF INVENTION: Detection of DNA Heteroduplex Molecules
TITLE OF INVENTION: Detection of DNA Heteroduplex Molecules
TITLE OF INVENTION: Detection of Comparative Sequencing
TITLE OF INVENTION: Methods for Comparative Sequencing
NUMBER OF SEQUENCES: 29
CORRESPONDENCES: 29
CORRESPONDENCES: 20
CITY: Palo Alto
SITRE: GA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MEZES, PETER S
APPLICANT: MEZES, PETER S
APPLICANT: RIXON, MARK W
APPLICANT: RIXON, MARK W
APPLICANT: RIXON, WH KERR
APPLICANT: SCHOLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
CORRESPONDENCE ADDRESS:
ADDRESSEE: DUANE C ULMER
STREET: P.O. BOX 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 9; DB 1; Length 22; 100.0%; Pred. No. 2.8e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STALL
COUNTRY: USA.
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,681
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, SUSAN T.
REFERENCE/DOCKET NUMBER: 8600-0155
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: ACID NO: 10:
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Patent No. 5993813
GENERAL INFORMATION:
APPLICANT: MEZES, PETER S
APPLICANT: GOURLIE, BRIAN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Gaps

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APPLICANT: GOUBLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: ANDERSON, WH KERR
APPLICANT: KAPLAN, DONALD A
APPLICANT: KAPLAN, DONALD A
APPLICANT: ACHOLOM, JEFFREY
APPLICANT: A NOVEL FAMILY OF HIGH AFFINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

100.0%; Score 9; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 9; DB 2; Length 22; Best Local Similarity 100.0%; Pred. No. 2.8e+03; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/479,285

FILING DATE: 07-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/040687

FILING DATE: 31-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: ULARS: DANE:

REGISTRENCE/DOCKET NUMBER: G-37,075C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 636-8104

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MICHIGAN
COUNTRY: USA
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 35, Application US/08479285 Patent No: 6207815 GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION: TELEPHONE: (414) 277-5000
                      TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5501
INPORMATION FOR SEQ ID NO: 240:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DUANE C ULMER
STREET: P.O. BOX 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                     1 ACAAATGTT 9
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JS-08-479-285-35
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1 ACAAATGTT 9

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March 25, 2004, 10:03:04; Search time 14.7262 Seconds (without alignments) 4297.861 Million cell updates/sec
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1. (cgn2_6/prodata1/) Pubpna/US07_PUBCOMB.seq:*

3. (cgn2_6/prodata1/) Pubpna/US06_NEW_PUB.seq:*

3. (cgn2_6/prodata1/) Pubpna/US06_NEW_PUB.seq:*

3. (cgn2_6/prodata1/) Pubpna/US06_PUBCOMB.seq:*

3. (cgn2_6/prodata1/) Pubpna/DS06_PUBCOMB.seq:*

3. (cgn2_6/prodata1/) Pubpna/DS06_PUBCOMB.seq:*

3. (cgn2_6/prodata1/) Pubpna/US08_PUBCOMB.seq:*

3. (cgn2_6/prodata1/) Pubpna/US08_PUBCOMB.seq:*

3. (cgn2_6/prodata1/) Pubpna/US08_PUBCOMB.seq:*

3. (cgn2_6/prodata1/) Pubpna/US09_PUBCOMB.seq:*

3. (cgn2_6/prodata1/) Pubpna/US09_PUBCOMB.seq:*

3. (cgn2_6/prodata1/) Pubpna/US09_PUBCOMB.seq:*

4. (cgn2_6/prodata1/) Pubpna/US09_PUBCOMB.seq:*

3. (cgn2_6/prodata1/) Pubpna/US108_PUBCOMB.seq:*

4. (cgn2_6/prodata1/) Pubpna/US108_PUBCOMB.seq:*

5. (cgn2_6/prodata1/) Pubpna/US108_PUBCOMB.seq:*

6. (cgn2_6/prodata1/) Pubpna/US108_PUBCOMB.seq:*

7. (cgn2_6/prodata1/) Pubbna/US108_PUBCOMB.seq:*

7. (cgn2_6/prodata1/) Pubpna/US108_PUBCOMB.seq:*

8. (cgn2_6/prodata1/) Pubpna/US108_PUBCOMB.seq:*

7. (cgn2_6/prodata1/) Pubpna/US108_PUBCOMB.seq:*

8. (cgn2_6/prodata1/) Pubpna/US108_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2458946 seqs, 1861504846 residues
                                                                                                                                                                                                                                                                                                                                                US-09-963-285-1_COPY_359_375
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_NA:*
                                                                                                                                           - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	QI	Description
	17	100.0	962	51	US-10-027-632-9718	Sequence 9718, Ap
N	17	100.0	6458	o	US-09-963-285-1	Sequence 1, Appli
m	16	94.1	493	12	US-10-424-599-107702	Sequence 107702,
4	16	94.1	2523	12	US-10-424-599-82796	Sequence 82796, A
n U	16	94.1	21619	10	US-09-764-891-10003	Sequence 10003, A
9	16	94.1	21619	14	US-10-205-428-977	Sequence 977, App
7	15.4	90.6	20	15	US-10-131-827-1138	Sequence 1138, Ap
œ	15.4	90.6		13	US-10-424-599-64036	Sequence 64036, A
σ	15.4	90.6	386	10	US-09-814-353-17187	Sequence 17187, A
10	15.4	90.6		12	US-10-424-599-22032	Sequence 22032, A
c 11	15.4	90.6	589	15	US-10-027-632-242033	Sequence 242033,
c 12	15.4	90.6	589	15	US-10-027-632-242034	Sequence 242034,
13	15.4	90.6		12	US-10-424-599-141232	Sequence 141232,
c 14	15.4	90.6		12	US-10-424-599-63676	Sequence 63676, A
ר ה	15.4	0	676		TIS-10-027-632-148185	Section 148185

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Gaps

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Query Match 100.0%; Score 17; DB 15; Length 962; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 17; Conservative 0; Mismatches 0; Indels (

1. TGTGGAAGGAATAATA 17

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Sequence 37752, A Sequence 43641, A Sequence 256262, Sequence 256263, Sequence 256264, Sequence 24, Appl Sequence 12, Appl Sequence 17, Appl Sequence 27, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 311, Appl Sequence 311	Sequence 1367, Ap Sequence 1367, Ap Sequence 1368, Ap Sequence 1368, Ap Sequence 1368, Ap Sequence 1468, Ap Sequence 17, Appli Sequence 659, Appli Sequence 6, Appli Sequence 1, Appli	le Nucleotide
12 US-10-424-599-37752 12 US-10-424-599-43641 15 US-10-622-556262 15 US-10-027-632-256263 15 US-10-027-632-256263 16 US-10-6628-95 17 US-10-087-080-24 18 US-10-229-345-12 19 US-10-34-434-17 15 US-10-087-080-27 15 US-10-087-080-27 16 US-10-087-080-27 17 US-10-087-080-27 18 US-10-087-080-27 19 US-00-963-285-5 14 US-10-221-613-351 14 US-10-221-613-351		ALIGNMENTS 127-528-9718 The 9718 ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS BEFREICH E. OF INVENTION: Identification and Mapping of Single BERT APPLICATION WINER: US 60/218,006 REPLING DATE: 2000-04-20 REPLING DATE: 2000-07-12 REPLING DATE: 2000-03-29 REPLING DATE: 2000-03-29 REPLING DATE: 2000-03-29 REPLING DATE: 2000-03-29 REPLING DATE: 1999-11-23 REPLING DATE: 1999-11-23 REPLING DATE: 1999-11-23 REPLING DATE: 1999-11-23 REPLING DATE: 1999-09-28 REPLING DATE: 1999-08-09
820 1228 1228 1228 1228 1238 2336 2336 2336 2336 2336 2336 2336 2	16281 16281 16285 16285 16285 16285 16285 17294 17294 17294 17294 180557 180557 180557 180557 180557 180557 180557	-62-9718 -9718, PRPHICALION US/10027 tion NG. USO030204075A9 ANT: WANG, David G. OF INVENTION: David G. OF INVENTION: David G. TAPPLICATION UNMER: US/10/ TAPPLICATION NUMBER: US 60/21 FILING DATE: 2000-07-12 APPLICATION NUMBER: US 60/19 APPLICATION NUMBER: US 60/19 FILING DATE: 2000-03-29 APPLICATION NUMBER: US 60/19 FILING DATE: 2000-03-29 APPLICATION NUMBER: US 60/19 FILING DATE: 1999-11-23 APPLICATION NUMBER: US 60/16 FILING DATE: 1999-11-23 APPLICATION NUMBER: US 60/16 FILING DATE: 1999-10-23 APPLICATION NUMBER: US 60/16 FILING DATE: 1999-10-28 APPLICATION NUMBER: US 60/16 FILING DATE: 1999-09-28 FILING DATE: 1999-09-28 FILING DATE: 1999-08-09 FILING DATE: 1999-08-09 FILING DATE: 1999-08-09 FILING DATE: 1999-08-09 NO 9718 H: 962 H: 962 IISM: Human -632-9718
		-632-9718 -6 9718 APPH tion No. US20 INFORMATION: OF INVENTION: OF INVEN
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Sequence 82796, Application US/10424599
Sequence 82796, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 36-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 82796
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10003
LENGTH: 21619
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Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT PILLING DATE: 2001-01-17
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Publication No. US20030108907A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 94.1%; Score 16; DB 12; I
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 0;
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US-10-424-599-82796
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                                                          233 GTGGAAGGAATAAATA 248
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Best Local Similarity 100.(
Matches 16; Conservative
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CRGANISM: Homo sapiens
US-09-764-891-10003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Glycine max
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US-09-764-891-10003/c
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Sequence 107702, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: Exer Areas Journal Journal
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100.0%; Score 17; DB 9; Length 6458;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: unsure at all n locations
FEATURE:
                                                                                                                                                   US-09-98-128-128-1
Sequence 1, Application US/09963285
Fatent No. US2002009707A1
GENERAL INFORMATION:
APPLICANT: Enerbock, Sven
APPLICANT: Krock, Katarina
APPLICANT: Wondan!, Lena
APPLICANT: Wondan!, Lena
APPLICANT: Wasserman, Wyeth
ITLE OF INVENTION: PROMOTER SEQUENCES
CURRENT APPLICATION NUMBER: US/09/963,285
CURRENT FILING DATE: 2001-09-26
PRIOR PILING DATE: 2000-11-09
PRIOR PILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PSECSEQ for Windows Version 4.0
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727 TGTGGAAGGAATAAATA 743
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; LOCATION: (2235)...(3737)
US-09-963-285-1
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ORGANISM: Homo sapiens
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US-10-424-599-107702
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GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38 –21(5323.8)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ENGITH: 359
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APPLICANT: Incline, James
ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
ITILE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT PELING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR PLICATION NUMBER: US 60/207,124
PRIOR FILING DATE: 2000-06-15
PRIOR PLICATION NUMBER: US 60/211,940
PRIOR PLICATION NUMBER: US 60/216,820
PRIOR PLICATION NUMBER: US 60/216,820
PRIOR PLICATION NUMBER: US 60/220,661
PRIOR PLICATION NUMBER: US 60/220,661
PRIOR PLICATION NUMBER: US 60/257,672
PRIOR PLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-25
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Pred. No. 8.1e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_28838C.1
MS-10-424-599-64036
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Publication No. US20030165831A1
GENERAL INFORMATION;
                                                                                                                                                                  Sequence 64036, Application US/10424599
Publication No. US20040031072A1
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94.1%;
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Best Local Similarity 94.1
Matches 16; Conservative
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ORGANISM: Glycine max
                                                                                                                                          -10-424-599-64036
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US-10-131-827-1138
i Sequence 1138, Application US/10131827
j Publication No. US20040009479A1
j FUBLICATION.
APPLICANT: Whilemuth, Jay
i APPLICANT: Whilemuth, Jay
i APPLICANT: Whilemuth, Jay
i APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
i APPLICANT: Woodward, Robert
i TILE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
TILE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
TILE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
TILE OF INVENTION: WHORER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
NUMBER OF SEQ ID NOS: 9990
software: Patentin Version 3.1
SEQ ID NO : 9890
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FILE REPERENCE: PA117C1

CURRENT APPLICATION NUMBER: US/10/205,428

CURRENT FILING DATE: 2002-07-26

PRIOR PILING DATE: 2001-01-17

PRIOR PILING DATE: 2001-01-17

PRIOR PILING DATE: 2000-01-31

PRIOR PILING DATE: 2000-02-34

PRIOR PILING DATE: 2000-02-34

PRIOR APPLICATION NUMBER: 60/180,628

PRIOR PILING DATE: 2000-06-28

PRIOR APPLICATION NUMBER: 60/214,886

PRIOR PILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 60/217,487

PRIOR PILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-07-14

PRIOR PILING DATE: 2000-07-11

PRIOR PILING DATE: 2000-07-14

PRIOR PILING DATE: 2000-07-14
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94.1%; Score 16; DB 14; Length 21619;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0;
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Pred. No. 6.5e+02;
0; Mismatches 1;
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Best Local Similarity 94.1%;
Matches 16; Conservative
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CONGANISM: Homo sapiens
US-10-205-428-977
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US-10-131-827-1138
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LENGTH: 21619
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Sequence 141232, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Xoalyina
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                 Length 589;
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                          Score 15.4; DB 15;
Pred. No. 8.5e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 242034, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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Matches 16; Conservative (
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US-10-027-632-242034/c
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US-10-027-632-242034
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: A Rovalic David K
APPLICANT: Cavalic David K
APPLICANT: Cavalic David K
APPLICANT: Cavalic David K
APPLICANT: Cavalic Sol Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Sol Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRESENCE: 38-21 (53-23)3
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/0218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-22
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 1099-102-8
PRIOR FILING DATE: 1099-102-8
PRIOR FILING DATE: 1099-102-8
PRIOR FILING DATE: 1999-103-8
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-09
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90.6%; Score 15.4; DB 12; Length 493;
Best Local Similarity 94.1%; Pred. No. 8.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0.
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US-10-424-599-22032
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OTHER INFORMATION: unsure at all n locations
FEATURE:
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ORGANISM: Glycine max
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US-10-027-632-242033/c
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; ORGANISM: Human
US-10-027-632-242033
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US-10-424-599-22032
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Length 676;
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Pred. No. 8.6e+02;
0; Mismatches 1;
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                                                                   Query Match 90.6%; Soc
Best Local Similarity 94.1%; Pre
Matches 16; Conservative 0;
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; ORGANISM: Human
US-10-027-632-148185
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US-10-424-599-63676/C

US-10-424-599-63676/C

Sequence 63676, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 63676

LENGTH: 616
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

PRIOR PELING DATE: 2000-04.30

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PELING DATE: 2000-03-29

PRIOR FILING DATE: 1999-113,83

PRIOR FILING DATE: 1999-103-83

PRIOR FILING DATE: 1999-103-83

PRIOR FILING DATE: 1999-103-83

PRIOR FILING DATE: 1999-09-28
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                                          90.6%; Score 15.4; DB 12; Length 606; ilarity 94.1%; Pred. No. 8.5e+02; Conservative 0; Mismatches 1; Indels 0
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US-10-424-599-63676
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 148185
LENGTH: 676
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US-10-027-632-148185/c
; Sequence 148185, Application US/10027632
; Publication No. US20030204075A9
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Best Local Similarity
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Human gen Human imm Prokaryot Human SQV Oligonucl Oligonucl Human GPC Human STA

Abq31996 Abq31996 Abq31997 Abq31997 Abq31997 Abq31997 Abq31997 Abq52496 Abq6215 Abq622577 Abq660227 Abq660

Human WNT Human WNT Oligonucl

Oligonucl

Human gen Human gen Human gen

Human

Run on:

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New construct comprising a human FOXC2 gene, useful in gene therapy for treating obesity- or malnutrition-related diseases (e.g. obesity or hyperlipidemia), as well as for identifying compounds useful in treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOXC2; human; winged helix protein; FKHL14; transcription factor; forkhead gene; energy balance; adipose tissue; transgenic animal; obesity; malnutrition; hyperlipidaemia; diabotes; hypertension; annidiabetic; anorectic; hypolipaemic; hypotensive; gene therapy; ss.
                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human winged helix protein FOXC2 cDNA.
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                                  ABQ31997
ABQ31994
ADA02552
ADB72290
ABQ52497
ABQ52496
AAC823975
ACA23975
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ABQ19255
ABQ19254
ADC86736
ADA02654
ADB72392
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26-MXA-2000; 2000SE-00001982.
06-JUN-2000; 2000US-00587945.
14-DEC-2000; 2000SE-00004629.
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Ada71938 Rice gene
Aak48768 Human FOX
Aax53491 Human ade
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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The present sequence is that of cDNA encoding human FOXC2 winged helix protein (see AAB82851). The cDNA was isolated from a human fat cell cDNA library using a mix of cDNA probes corresponding to DNA-binding domains from different winged helix proteins. FOXC2 (also designated FKHI14) was corresponded to the genes identified. Northern blotting showed FOXC2 to be corresponded to the genes identified. Northern blotting showed FOXC2 to be corresponded for identified. Northern blotting showed FOXC2 to be corresponded for regulating energy balance and adiposity was demonstrated. The invention provides transgenic non-human mammals that are capable of expressing the human FOXC2 gene in their adipose tissue. Methods are corrected for identifying compounds useful for the treatment of medical conditions related to obesity, such as obesity, non-insulin dependent conditions related to obesity, such as obesity, non-insulin dependent stimulate the biological activity of a human FOXC2 polypeptide. Methods are stimulate the biological activity of a human FOXC2 polypeptide. Methods are also provided for identifying compounds useful for the treatment of medical conditions related to malnutrition, such as anorexia (claimed). Such compounds decrease human FOXC2 gene expression or FOXC2 protein conditions related to malnutrition, such as anorexia (claimed).
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GGAAATCTAATTACGCTTCATCACTCATTAATAAGAAAATGTCCCAGGATCATTGCT 120
                                            121 ACTIACAAGGICTITIGGGAGAGATATITIACICTATIAATCCATICTATITIATATITACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes an isolated human FOXC2 promoter region. The mammalian FOXC2 promoter region for the modulation of FOXC2 polypeptide expression has therapeutic value in treating type II diabetes mellitus, obseity, hypercholesterolaemia, other cardiovascular diseases or dyslipidaemias. This sequence encodes the human transcription factor FOXC2, the promoter of which is described in the invention
                                                                                                                             form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression of a
type II diabetes
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'note≈ "Portion of polypeptide used in alternative
                      the alternative
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100.0%; Score 986; DB 6;
Best Local Similarity 100.0%; Pred. No. 2e-202;
Matches 986; Conservative 0; Mismatches 0;
                                                                                                                                                                                          /product= "FOXC2"
/note= "Transcription factor"
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/*tag= "Region coding for DNA-b.
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  claimed in claim
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2000US-0238897P.
2000SE-00004102.
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3741. .4629
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P-PSDB; AAU79816.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATGTGATAATAAATTAAAATTTTATAAGATGTAACTCATTTTTAAAAGTCCTCAAGTTA 1444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an isolated human FOXC2 promoter region. The mammalian FOXC2 promoter region for the madulation of FOXC2 polypeptide expression has therapeutic value in treating type II diabetes mellitus, obesity, hypercholesterolaemia, other cardiovascular diseases or dyslighdaemias. This sequence encodes the mouse mesenchyme forkhead 1 (MHF-1) protein (also called FOXC2 transcription factor), described in the method of the invention
                                      Transcription factor; FOXC2; antidiabetic; anorectic; antilipaemic; cardiovascular; FOXC2 polypeptide expression modulator; FOXC2 promoter; diabetes mellitus; obesity; hypercholesterolaemia; dyslipidaemia; cardiovascular disease; mouse medenchyme forkhead 1; MHF-1; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1145 TITGCTCTGAACCCATTACAACTAGGCCCCGATAATTAAGAAATCTAATTATTCGCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1205 TCATCCATTAATAATAAAAAAAAAATCTCCAGGCTCTTTCCTACTTACAAGGTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated FOXC2 promoter region that modulates the expression of a FOXC2 polypeptide is useful for treating obesity and type II diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 TCACTCATTAAT-----AAGAAAATGTCCCAGGATCATTGCTACTTACAAGGTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGAGAGATATTTTACTCTATTAATCCATTCTATTTTATATTTCAAATTGA-----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1265 GGGGGAAATCTCTGCCCAACTTCATCAATTCGATGTTATATTTCAAACTAAACTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITITITAACAGAAAAGTGGCTATCTTTTTGGGCATGTGGGCCATTCACCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 INGCITITGAATCCATTACACCTGGGCCCCCATAATTAGGAAATCTAATTATTCGCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Genomic DNA encoding mouse mesenchyme forkhead-1 (MHF-1)/FOXC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6021 BP; 1350 A; 1675 C; 1642 G; 1354 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                     /product= "MHF-1 or FOXC2"
/note= "Mouse mesenchyme forkhead 1"
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Pred. No. 1.4e-52;
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                                                                                                                                                                                     Location/Qualifiers
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10-OCT-2000; 2000US-0238897P.
09-NOV-2000; 2000SE-00004102.
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Best Local Similarity 64.9%;
Matches 597; Conservative
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P-PSDB; AAU79818.
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The present invention relates to a method of identifying RNA-binding molecule comprising predicting the structure of RNA-fragment, selecting suitable predicted RNA fragment with an individual stem, synthesising a DNA-fragment corresponding to the RNA fragment, inserting the DNA fragment in upstream proximity of reporter assay gene to form reporter construct and performing a reporter gene assay which detects interaction between a molecule to be tested for RNA-binding and RNA fragment of the reporter construct. The method is useful for identifying an RNA binding is used to illustrate the method of the invention
Identifying RNA-binding molecule by predicting structure of RNA fragment, synthesizing DNA fragment corresponding to predicted RNA structure, performing reporter gene assay after placing the DNA upstream of reporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 125 BP; 7 A; 65 C; 32 G; 0 T; 21 U; 0 Other;
                                                                                                                               29; 35pp; English
                                                                                                                               Page
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                                                                    GCCCCCTCGCTCCCCCGGCGCAGTCCGTGCGCGAGGCCGCCGAGCCGTCTCGGAA 980
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                                  CCGCCCCTCCCGCTCCCCTCTCCCCCTCTGGCTCTCTGGCGCTCTCTCGCTCTCAGG
                                             Gaps
                   .
 Length 125;
                 0; Indels
, DB 7;
1.6e-17;
                21; Mismatches
12.7%; Score 125;
83.2%; Pred. No. 1
                 Matches 104; Conservative
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Query Match
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2000
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                                                  DNA;
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                                                  standard;
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BP.

bacterial infection; fungal infection; viral infection; rice; Plant; gene;

WO2003000898-A1 Oryza sativa

03-JAN-2003

22-JUN-2001; 2001WO-IB001105

22-JUN-2001; 2001WO-IB001105

Hou Y; T, Zou SA, Zhu Goff. J, G Xie Glazebrook Whitham S, (SYGN) SYNGENTA PARTICIPATIONS יל מ Cooper Chen W, Co Ľ, Chang H, Katagiri

ö

WPI; 2003-175290/17.

t 0 Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant expression gene

NO 5263; 899pp; English Claim 27; SEQ ID

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          The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly attered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
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                                                                                                                                                                                                                                                                                                         65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YCWYYYYGMYMKCSYMMRYGYCKACKKCCYAMCWKAAYSGMMYYWYKKYSKWMRMSTKYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 MRKKTKYSKRCYCWRYATCYWCCCYRKRGWYSRRSWMRTAGKWKMRSWSRWCRSYSWYKM
                                                                                                                                                                                                                                                                                                                           TCTAATTATTCGCTTCATCACTCATTAATAAGAAAATGTCCCAGGATCATTGCTACTTA
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                                                                                                                                                                                                                                                                                                         6 ATTCCAATCCAGCGCGTTTGCTTTTGAATCCATTACACCTGGGCCCCCATAATTAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                925 SCMWWKYWRIWSCWY--IMWWGAMRYAYYAMRRRRWIYKWSWRRMYWIWIKWAWIWMICM
                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAGGICTITGGGAGAGATATTTTACTCTATTAATCCATTCTATTTTATATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              543 CGGACCCCGGCGCGCTGACCCTCGGGGCTGCCGATTC-GCTGGGGGCTTGGAGAGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGGGGCCGGCGGCTGCGCTTGCCCCGGGCGCGCCCTCCAGGATGCCGATCCGCCCGGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCGCCCCTCCTCGCGCGGGCCGAGGGTCCACCTTGGTCCCCAGGCCGCGGCGTCTCCGC
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                                                                                                                                                                                                                                      Length 2000;
                                                                                                                                                                                                   Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                        412;
                                                                                                                                                                                                                                  Query Match

8.1%; Score 79.8; DB 7;

Best Local Similarity 10.0%; Pred. No. 1.9e-07;

Matches 98; Conservative 460; Mismatches 412;
                                                                                                                                                                 illustrate the invention.
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Human adenosine Al receptor antisense oligonucleotide fragment.

(first entry)

05-JUL-1999

AAX53491;

AAX53491 standard; DNA; 114955

RESULT 7 AAX53491

61 GCGCGAGGGCGCCGG 75

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The present invention relates to a method of identifying RNA-binding molecule comprising predicting the structure of KNA-fragment, selecting suitable predicted RNA fragment with an individual stem, synthesising a DNA-fragment corresponding to the RNA fragment, inserting the DNA fragment in upstream proximity of reporter assay gene to form reporter construct and performing a reporter spene assay which detects interaction between a molecule to be tested for RNA-binding and RNA fragment of the reporter construct. The method is useful for identifying an RNA binding molecule. The present sequence is human FOXC2 RNA fragment. This sequence is used to illustrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying RNA-binding molecule by predicting structure of RNA fragment, synthesizing DNA fragment corresponding to predicted RNA structure, performing reporter gene assay after placing the DNA upstream of reporter
                                        GWKWRSKYSMCCKKYCSCTKYCSYTGYRRYCKWYKYSYYKCYYCYCYWYMSYMRKC 89
                                                                                                                                                                         |: | :::: | :::: | :::: | |: | |::: | |::: | | |::: | | |::: | | |::: | | |::: | | |::: | | |::: | | |::: | | |::: | | |::: | | |::: | | |::: | | |::: | | |::: | | |::: | | |::: | | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: |:: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |:: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |:: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |:: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |
GCGCTCTCTCCCCTCTCAGGGCCCCCCCCCCCCCCCGGCCGCAGTCCGTGCGCGAGGGCG
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Pred. No. 8 4e-07;

Or Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; RNA binding molecule; FOXC2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 29; 35pp; English.
                                                                                                                                                                                                                                                                         962 CCGGCGAGCCGTCTCGG 978
                                                                                                                                                                                                                                                                                                                 SKKCTKRKYYYCYWSSG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD48768 standard; RNA; 75 BP
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Best Local Similarity
Matches 62; Conserv
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                                                                                                                                    902
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ID AAD
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The specification describes antisense oligonucleotides (AAX52869-X55271).

directed against at least 2 mRNAs selected from target genes, coding and concoding regions of RNAs corresponding to target genes, gene initiation codins, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense cligonucleotides may be derived from sequences AAX55272-74. These multiple target oligonucleotides from sequences AAX55278-271 and be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vascoonstriction, inflammation, including lung distances syndrome, pain, cystic fibrosis, pulmonary hypertension distances syndrome, pain, cystic fibrosis, pulmonary wascoonstriction, emphysema, chronic obstructive pulmonary classes (COPD), and cancers such as leukemias, lymphonas, carcinomas e.g. colon cancer, breast cancer, lung cancer, melasnoma, hepatic metastasized to the lungs, including breast and prostate cancer.
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                                                                                                                                  Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasconstration; inflammation, allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pencreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense oligonucleotides used in treatment of, e.g. pulmonary
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7.6%; Score 74.8; DB 2; Length 1:
Best Local Similarity 34.7%; Pred. No. 7.2e-06;
Matches 168; Conservative 58; Mismatches 257; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 37; 120pp; English.
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98US-00093972.
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                                                                                                                                                                                                                                                                                                                              prostate cancer; ss
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Gaps ; 0 9

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891 CTGGCTCTCTCGCGCTCTCTCGCTCTCAGGGCCCCCCTCGCTCCCCCGGGCGCAGTCGGT

Pred. No. 8.46

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The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
                                                                                                                                                                                                                                                                                                                                                                                      721 AGCGGGCCGGCGCTGCGCTTGCCCGGGGGGCGCCTCCAGGATGCCGATCCGCCCGGTC 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 CTCGGACCCCGGCGCGCTGACCCTCGGGGCTGCCGATTCGCTGGGGGCTTGGAGAGCCTC
                                                                                                                                                                                                                                                                  CNININININCNCACHCUCCLTINICUCNINININININININGCUNINIANINININININICCTCCCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCGCTCTCTCGCTCTCAGGGCCCCCTCGCTCCCCCGGGCCGCAGTCCGTGCGCGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, cytosine methylation, 5'-Cpd-3'; uracil; cytosine, diagnosis; drug; side effect, cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide for detecting cytosine methylation SEQ ID NO 5817
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                                                                                                                                            Sequence 1117 BP; 143 A; 72 C; 471 G; 123 T; 0 U; 308 Other;
                                                                                                                                                                                                        0; Mismatches 279; Indels
                                                                                                                                                                          Score 73; DB 9; ]
Pred. No. 4.8e-06;
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ABO19226/c
TD ABQ19226 standard; DNA; 687
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Matches 157; Conservative
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                                                                                                                                   GGCGCCGCCGCCGGCCGGSNNNDNNBGGGCGCCGCCGCCGGGCCGSNNNDNNGG 105201
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                                                                                                                                                                                                     GGGACTTGGCCTCTTTTTCTGGGCTCAGCGGGGAGCCGCTCGGACCCCGGCGCGCTGAC
                                                                                                                                                                            TGCCCGCGCTGCCGCCGCCGGGTCCTGGAGCCAGCGAGGAGCGGCGCCGCCGCCTGCGCTT
                                                                                                                                                                                                                                   105022 CGGCCGGGCCGSNNNDNNGGCCBGGGCGCGCCGCCGGCCGGGCCGGSNNNDNNGCCBGGGC
                                                                                                                                                                                                                                                                                                                                                                                    105082 GCGCCGCCGGCCGGGCCGSNNNDNNCCBGGGCGCGCCCGGCCCGGGCCGSNNNDNNCBG
                                                        CCTCGGGGGCTGCCGAITCGCTGGGGGCTTGGAGAGCCTCCTGCGCCCCCTCCTCCTCGCGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                  922 CCCCCCTCGCTCCCCCGGGCCGCAGTCCGTGCGGAGGGCGCCGGCGGCGGCGGTCTCGGAAG
                                                                                                                CTCGGCCCGAGGACGACGACGCGCACCTCGCCCCGGAGGCTGCCAGGAGACCGGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  triphosphate-binding protein coupled receptor; gene therapy
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(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1141; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human GPCR gene SEQ ID NO:1141
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P-PSDB; ADC86689.
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ADC86688 standard;
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499 960 439

05-SEP-2000; 2000DE-01044543.

(EPIG-) EPIGENOMICS AG

Ä Guetig

Berlin K,

Piepenbrock C,

olek A,

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convext cytosine (C) but not methylated C, to uracil, then part of the genomic contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligomers in the range of publication to both classes, each with at least one member, of oligomers. From the ratio of labels hybridised to the two classes of cligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc. particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously, ABQ13410-ABQ5412 represent genomic DNA sequences used to illustrate the method for disclosure of the invention
                                                                                                                                                                                            Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons
                                                                                                                                                                                                                                                                                             Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                      diagnosis and prognosis, con
from chemically treated DNA.
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Sequence 687 BP; 11 A; 123 C; 446 G; 88 T; 0 U; 19 Other;

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                                                                     CCTCCTGCGCCCCTCCTCGCGGGGCGGAGGTCCACCTTGGTCCCCAGGCCGCGGGGTC 656
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                                                                                                      514 CCCCCCGCGCCCCGGACGCCCCCGCCCCGAACGCGAACCCGCCCCGACGCCGANAC
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                                  Gaps
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'Match 7.1%; Score 70; DB 6; Length 687; Local Similarity 48.7%; Pred. No. 1.9e-05; les 175; Conservative 0; Mismatches 184; Indels
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ABQ19227 standard; DNA; 687

(first entry)

12-JUL-2002

ABQ19227;

RESULT 10
ABQ19227
ID ABQ19;
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a morif 5-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert of cytosine (C) but not methylated (', to uracil', then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptides-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on clasmes, the degree of methylation is calculated. The method is used of ignmers, the degree of methylation is calculated. The method is used of the amplicon. The diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastroinestinal and respiratory systems etc. particularly by detecting mutations or single nucleotide polymorphisms ('NP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation and the proposal of the central of many C residues to be determined similar the methylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 gececegaaceconnegaececegaacecegecegececececegaaaaceganneece
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                 Oligonucleotide for detecting cytosine methylation SEQ ID NO 5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 687;
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05-SEP-2000; 2000DE-01044543.
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                                                                                                                                                             Homo sapiens.
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The specification describes antisense oligonucleotides (AAX52869-X55271)
directed against at least 2 mRAAs selected from target genes, coding and
non-coding regions of RNAS corresponding to target genes, coding and
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
end and the juxta-section between coding and non-coding regions and all
segments of RNAs encoding proteins associated with one or more diseases,
conditions or mixtures. The antisense oligonucleotides may be derived
from sequences AAX5572-74. These multiple target oligonucleotides
conditions or mixtures. Typical diseases and conditions are those
specifically AAX5180-271) can be used for the antisense treatment of
diseases and conditions. Typical diseases and conditions are those
associated with impaired respiration and inflammation, including lung
diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
acute asthma, allergies, asthma, impeded respiration, respiratory
distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
colon cancer, breast cancer, lung cancer, melanoma, hepatic metastasses, as
well as all types of cancer which may metastasize or have metastasized
to the lungs, including breast and prostate cancer
CCGGAGGCTGCCAGGAGCCGGGCCGCCCTCCCGCTCCCCTCCTCCCCCTCTCTGGCT 896
                                                                 canacide ececedes es es estados estado
                                                                                                                                                                                                               pulmonary hypertension; pulmonary vasoconstriction; emphysema; carcinoma; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                              New antisense oligonuclectides used in treatment of, e.g. pulmonary vasoconstriction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human adenosine Al receptor antisense oligonucleotide fragment
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98US-00093972.
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09-JUN-1998;
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                                                                                                                                               10561 GGGCAAGCCGGGGCCGAGGCCGAGGCCGAGGGCCCNNHNNNSCGGGCCGGGCGGGCAAGC 105602
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                                                                                                                523 GGCTCAGCGGGGCAGCCGCTCGGACCCCGGCGCGCTGACCCTCGGGGCTGCCGATTCGCT 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the
            Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 0 U; 21427 Other;
                                                                                                                                                                                                                                                                          105541 CGGGGCCGAGCCAGGGGCCCNNHNNNSVGCGGAGCCVGCGCCCCNNHNNNSCGGCCCGCC
                                                                                                                                                                                 GOGGGCTTGGAGAGCCTCCTGCGCCCCTCGCGCGGGGCCGAGGGTCCACCTTGGTCCC
                                                                                                                                                                                                                                                 763 ATGCCGATCCGCCCGGTCCGCTGAAAGCGCGCCCCTGCTCGGCCCCGAGCGACGAC
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guanosine triphosphate-binding protein coupled receptor; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          883 CTCCCCCTCTGGCCTCTCTCGCGCTCTCTCGCTCTCAGGGCCCCCCTCGCTCCCCCGGCCG
                                            Length 114955;
                                            Query Match 7.0%; Score 69.4; DB 2; Sest Local Similarity 37.0%; Pred. No. 0.0001; Matches 166; Conservative 25; Mismatches 258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          943 CAGTCCGTGCGCGAGGGCGCCGGCGAGCC
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                                   The invention relates to a novel polynuclectide encoding a guanosine triphosphare-binding protein coupled receptor (GPCR). A polynuclectide of the invention may have a use in gene therapy. The polynuclectide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynuclectide sequences shown in ADC85548-ADC87616 encode GPCR's of the
                                                                                                                                                                                                                                                                                                                                          CCGGAGGCTGCCAGGAGACCGGGCCGCCCTCCCGCTCCCCTCTCCCCTCTGGCT 896
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                                                                                                                                            Length 3163;
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detection; cancerous state; metastasis; identification; bro
oestrogen receptor-positive breast cancer; therapy;
oestrogen receptor-negative breast cancer; lung cancer; ss.
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guanosine triphosphate-binding protein coupled receptor
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Pred. No. 4.2e-05;
                  Claim 1; SEQ ID NO 1513; 28pp; English
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15-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in comprising sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-
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J, Innis MA, Garcia PD, Sudduth-Klinger J;
Randazzo F, Kennedy GC, Pot D, Kassam A;
Crkvenjakov R, Dickson M, Drmanac S, Labat I;
Garcia V, Jones LW, Stache-Crain B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1000;
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       Williams LT, Escobedo
Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-126369/11.
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Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons
        Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                       Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                               Guetig
                                                                                                                                                                               Berlin K,
                                                                                                                               2000DE-01043826.
2000DE-01044543.
                                                                                                             01-SEP-2001; 2001WO-EP010074
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from chemically treated DNA.
                                                                                                                                                                               Piepenbrock C,
                                                                                                                                                           (EPIG-) EPIGENOMICS AG
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                                                                         WO200218632-A2
                                                                                                                               01-SEP-2000;
05-SEP-2000;
                                                       Homo sapiens.
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3' present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and or avide and or prognosis of side effects of therapeutic drugs of oligomers, the degree of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP, s), and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously, ABQ13410-524 GCTCAGCGGGGCAGCCGCTCGGACCCCGGCGCGCTGACCCTCGGGGCTGCCGATTCGCTG 583 GOGGCTTGGAGGCCTCCTGCCCCC - - CTCCTCGCGCGGGCCGAGGGTCCACCTTGGTC 640 cciccio de de contra de co GGGTCTTGGAGCCAGCGAGGAGGGGGCCGGCTGCGCTTGCCCGGGGGGCGCCCTCCA 760 761 GGATGCCGATCCGCCCGGTCCGCTGAAAGCGCGCGCCCCTGCTCGGCCCGAGCGACGACGACG 820 ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention 3; Score 68.4; DB 6; Length 712; Pred. No. 4.1e-05; 0; Mismatches 217; Indels Sequence 712 BP; 47 A; 456 C; 181 G; 12 T; 0 U; 16 Other; 6.9%; al Similarity 48.6%; 208; Conservative (320 380 260 584 Query Match Best Local 641 701 Matches g g g 임

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert genomic sample for methylated C, to uracil, then part of the genomic convert.

The amplicon is hybridised to two classes, each with at least one member, of oligomucleotides and/or peptide-nucleic acid (PNA) oligomers and the amplicon. From the ratio of lasses is determined from the label on the amplicon. From the ratio of lasses is determined from the label on clasmers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therappettic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastroinestinal and respiratory systems etc. particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation and analyses of status of many C residues to be determined simulated the methylation and analyses.
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                                                                                                                                                                     ABG54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the
821 ACCGCGCACCCTCGCCCCCGGAGGCTGCCAGGAGCCGGGGCCGCCCCTCCCCTC
                                                                                                                                 CTCTCCCCCTCTGGCTCTCTCGCGCTCTCTCAGGGCCCCCCTCGCTCCCCCGGGC
                                                                                           Human, cytosine methylation, 5'-CpG-3', uracil; cytosine, diagnosis, drug, side effect, cancer, central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
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05-SEP-2000; 2000DE-01044543.
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from chemically treated DNA.
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6.9%; Score 68.4; DB 6; Length 712;
Best Local Similarity 48.6%; Pred. No. 4.1e-05;
Matches 208; Conservative 0; Mismatches 217; Indels
                                                                                                          Sequence 712 BP; 12 A; 181 C; 456 G; 47 T; 0 U; 16 Other;
disclosure of the invention
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Sequence 50, 1
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Sequence 1, 2
Sequence 2, 3
Sequence 4, 3
Sequence 4, 3
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Sequence 10,
Sequence 13,
Sequence 7,
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Sequence 35,
Sequence 14,
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Sequence 3,
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                Issued_Patents_NA:*
1: /cgT2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgT2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgT2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgT2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgT2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgT2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-616-289-48
US-09-165-264-10
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US-09-616-289-45
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FALLIN NO. OLIVORA

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FILE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 09404/05201

CURRENT APPLICATION NUMBER: US/09/128,155

CURRENT PAPLICATION NUMBER: US 60/091,650

EARLIER FILING DATE: 1998-08-03

EARLIER FILING DATE: 1998-09-03

EARLIER FILING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 18

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6.1%; Score 59.8; DB 3; Length 152331;
Best Local Similarity 50.6%; Pred. No. 0.00041;
Matches 169; Conservative 0; Mismatches 163; Indels 2;
                  Sequence 16, Application US/09128155 Patent No. 6117654
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LCCATION: (1)...(153331)

/ OTHER INFORMATION: n = A,T,C or G

US-09-128-155-16
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ORGANISM: Homo sapiens
FEATURE:
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APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Ariora APPLICATION: PATHEROSCIEROSIS
FILE OF INVENTION: ATHEROSCIEROSIS
FILE REFERRNCE: 10797-004001
CURRENT APPLICATION NUMBER: US 09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-03-02
PRIOR PILICATION NUMBER: US 60/931,930
PRIOR PILICATION NUMBER: US 60/031,930
PRIOR PLILIATION NUMBER: US 60/031,930
PRIOR PLILIATION NUMBER: US 60/031,930
PRIOR PLILIATION NUMBER: US 60/048,547
PRIOR PLILIATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
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945 GICCGIGCGCGAGGGCGCCGCGAGCCGICICGG 978
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US-09-91-211-10
'Sequence 10, Application US/09791211
'Patent No. 6448080
                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/09616289
Patent No. 6632923
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Matches 180; Conservative
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/ LOCATION: (246)...(1895)

US-09-616-289-48
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GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andraw T. Wart
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
LENGTH: 98844
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Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INFORMION: Wilti-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEG ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.0%; Score 58.8; DB 4;
52.9%; Pred. No. 0.00059;
tive 0; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 64383
OTHER INFORMATION: unknown NAME/KEY: unsure
LOCATION: 65468
OTHER INFORMATION: unknown NAME/KEY: unsure
LOCATION: 65469
OTHER INFORMATION: unknown NAME/KEY: unsure
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LOCATION: 87130
OTHER INFORMATION: unknown
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LOCATION: 89049
OTHER INFORMATION: U
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OTHER INFORMATION:
NAME/KEY: unsure
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OTHER INFORMATION:
NAME/KEY: unsure
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OTHER INFORMATION:
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Matches 126;
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
ALITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCIEROSIS
TITLE OF INVENTION: ATHEROSCIEROSIS
FILE REFERENCE: 10797-004007-14
FILE REFERENCE: 10797-004007-14
FRIOR PELICATION NUMBER: US 09/517,849
FRIOR APPLICATION NUMBER: US 09/517,849
FRIOR FILING DATE: 1997-11-26
FRIOR FILING DATE: 1997-11-26
FRIOR FILING DATE: 1997-11-27
FRIOR PELICATION NUMBER: US 60/031,930
FRIOR PELING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
LEAST AND AST 
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                                                                                                                                                               Query Match

5.7%; Score 56.6; DB 4; Length 1614;

Best Local Similarity 47.5%; Pred. No. 0.00039;

Matches 200; Conservative 0; Mismatches 219; Indels 2;
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                                                                                                                                                                                                                                                                                                                      881 CICICCCCTCTGGCTCTC 899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                               FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-13
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                  Length 320;
                                                                                                                                                                                                                                                                                                                  Score 57.2; DB 3; Length 3
Pred. No. 0.00015;
0; Mismatches 163; Indels
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Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Ulnayagemoorthy, Thuraiayah

TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747

CURRENT APPLICATION UNMER: US/09/165,264

CURRENT APPLICATION UNMER: 1998-10-01

NUMBER OF SEQ ID NOS: 14

SOOTWARE: Patentin Ver. 2.1

SEQ ID NO 7

LENGTH: 320
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                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 48.7%;
Matches 155; Conservative
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US-09-165-264-7/c
        SEQ ID NO 13
LENGTH: 320
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A OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-8
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APPLICANT: Leopardi, Bernard
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 AS AN
TITLE OF INVENTION: INHIBITOR OF APOPTOSIS
NUMBER OF SEQUENCES: 2
CORRESSONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT PAPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
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; Sequence 1, Application US/08690473
; Patent No. 587623
; GENERAL INFORMATION:
                                                                                                                                                                                                                        US-09-165-264-8/c
; Sequence 8, Application US/09165264
; Patent No. 6197510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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Matches 152; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Houston
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Best Local
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                                                              TGGCTCTCTCTCGCGCTCTCTCGCTCTCAGGCCCCCCTCGCTCCCCCGGGCCGCAGTCCGTG 951
                                                                                                                          622 gadócgcygetrgecégéngeoddeaagecgeodgeoddeacacadadageageodgeod 681
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Sequence 50, Application US/09616289
Patent No. 6613293
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
TITLE OF INVENTION: PROTIENS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: PROTIENS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: PATHEROSCIEROSIS
TITLE OF INVENTION: PATHEROSCIEROSIS
FILE REPERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US 09/517,849
PRIOR PLILING DATE: 2000-07-14
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-27
PRIOR PRILING DATE: 1997-11-27
PRIOR PRILING DATE: 1997-11-27
PRIOR PRILING DATE: 1997-6-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSED for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                            952 C 952
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; TYPE: DNA; ORGANISM: HERPES VIRUS, TYPE US-09-259-821A-1
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COUNTRY: United States
                                                                                            Query Match
Best Local Similarity
Matches 178; Conserv
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APPLICANT: LEOPAZDI, ROSARIO
APPLICANT: LEOPAZDI, ROSARIO
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS
TITLE REFERENCE: ARCD:317
CURRENT APPLICATION NUMBER: US/09/259,821A
CURRENT FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 08/690,473
PRIOR FILING DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
LENGTH: 4257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   720 GAGCGGGGCGCCGCTGCGCTTGCCGGGGCGCGCCCTCCAGGATGCCGATCCGCCCGGT 779
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Best Local Similarity 46.5%; Pred. No. 0.0014;
Matches 178; Conservative 0; Mismatches 205; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,473
FILING DATE: 26-JUL-1996
CLASSIFICATION: 435
ATYONEY/AGENT INPORMATION:
REGISTRATION NUMBER: 37,642
REPERENCE/DOCKET NUMBER: 37,642
REPERENCE/DOCKET NUMBER: 37,642
TELEPHONE: 512/448-3000
TELEPHONE: 512/418-3000
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// Patent No. 6210926
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TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
ILENGTH: 4257 base pairs
TYPE: mucleic acid
STRANDENNESS: single
TOPOLOGY: linear
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US-09-259-821A-1
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                                                                                                                                                                                  720 GAGCGGGGCGGCTGCGCTTGCCCGGGGCGCGCCCTCCAGGATGCCGATCCGCCGGT
                                                                                                                           600 CCTGCGCCCTCCTCGCGCGGGCCGAGGGTCCACCTTGGTCCCCAGGCCGCGGGGGTCTCC
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      Length 4257;
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APPLICANT: Leopardi, Bernard
APPLICANT: Roizman, Bernard
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
5.6%; Score 55; DB 3; Length 425 ilarity 46.5%; Pred. No. 0.0014; Conservative 0; Mismatches 205; Indels
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COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FIRM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: CONCURRENT HEREWITH
CLASSIFICATION: 435
CLASSIFICATION: 435
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NAME: Highlander, Steven L.
REGISTATION NUMBER: 37,642
REPRENCE/DOCKET NUMBER: AKSB:519
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-757
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2724 CGCCGCGCGCAGGCCCGCCCGC 2746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCCGGCGAGCCGTCTCGGAAGC 982
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Patent No. 6218103
GENERAL INFORMATION:
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ORGANISM; Herpes simplex virus
STRAIN: Herpes Simplex Virus Type 1
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US-09-165-264-11/C
Sequence 11, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                   (215) 568-3100
                                                 TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 12001 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 48.5%;
Matches 150; Conservative
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                                                                                                                                                                                                 : 12001 base pairs
nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE:
                   TELEPHONE:
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US-08-458-568A-11/c
US-08-458-568A-11/c
Sequence 11, Application US/08458568A
Factor No. 5821339
GENERAL INFORMATION:
APPLICANT: Scheffer, Priscilla A.
APPLICANT: Yeh, Lily
TITLE OF INVENTION:
TITLE OF INVENTION: Infections
TITLE OF INVENTION: Infections
MUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
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                                                                                                                                                                                                                                                        Length 4257;
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Pred. No. 0.0014;
0; Mismatches 205; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,568A
FILING DATE: 02-JUNE-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,146
FILING DATE: 05-MAY-1993
CLASSIFICATION: 435
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NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
REPERENCE/DOCKET NUMBER: DFCI-0029
TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 46.5%;
Matches 178; Conservative
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                US-08-843-659-1
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                                                                                                                    600 CCTGCGCCCTCGCGCGGGCCGAGGGTCCACCTTGGTCCCCAGGCCGCGGGGGTCTCC
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Ouery Match 5.6%; Score 55; DB 1; Length 12001; Best Local Similarity 46.5%; Pred. No. 0.0021; Matches 178; Conservative 0; Mismatches 205; Indels
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Pred. No. 0.00062;
0; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Vinayagamoorthy, Thuraiayah TITLE OF INVENTION: Multi-Loci Genomic Analysis FILE REFERENCE: 44747 CURRENT APPLICATION NUMBER: US/09/165,264 CURRENT FILING DATE: 1998-10-01 NUMBER OF SEQ ID NOS: 14 SOFTWARE: Patentin Ver: 2.1 LENGTH: 320
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350 AGCCGGCGCCCTCGTCCTCGCTCAGCTAGAGACTCACGCTGGGCCCCCGCGGAAGCCGAC 291
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                            Sequence 7, Application US/08335865J
Patent No. 6107472
GENERAL INFORMATION:
APPLICANT: Stacker, Steven A.; Hovens, Christopher M.,
APPLICANT: Wilks, Andrew F.
TITLE OF INVENTION: RECEPTOR-TYPE TYROSINE KINASE-LIKE MOLECULES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 KB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII/Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,865J
FILING DATE: 19-January-1995
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REFERENCE/DOCKET NUMBER: LUD-52
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
FILING DATE: 10-May-1993
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
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STREET: 666 Fifth
CITY: New York
STATE: New York
COUNTRY: USA
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Matches 167; Conserva
     US-08-335-865J-7/c
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Best Local S
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US-09-165-264-12
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48.7%; Pred. No. 0.00069;
tive 0; Mismatches 156; Indels
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Patent No. 6197510
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747

CURRENT APPLICATION NUMBER: US/09/165,264

CURRENT FILING DATE: 1998-10-01

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Artificial Sequence
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LENGTH: 318
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Job time : 200.942 secs

Sequence 10475, A Sequence 10475, A Sequence 133788, Sequence 21, Appl Sequence 29, Appl Sequence 20495, A Sequence 20495, A Sequence 20495, A Sequence 20495, A Sequence 1191, Appl Sequence 16, Appl Sequence 48, Appl Sequence 2320, Appl Sequence 3350, Appl Sequence 6, Appl Sequence 3350, Appl Sequence 3350, Appl Sequence 3350, Appl Sequence 6, Appl

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100.0%; Score 986; DB 9; Length 3289;
Best Local Similarity 100.0%; Pred. No. 1.38-241;
Matches 986; Conservative 0; Mismatches 0; Indels 0;
US-09-954-456-292
US-09-954-456-529
US-09-880-107-3950
3 US-10-026-188-6
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JEGURERO 8, Application US/09963285

PATELICANT: UNCORMATION:
APPLICANT: Enerbock, Sven
APPLICANT: Enchock, Sven
APPLICANT: Enchock, Sven
APPLICANT: Rondahl, Hena
APPLICANT: Rondahl, Weth
TITLE OF INVENTION: PROMOTER SEQUENCES
FILE REPERENCE: 13425-04201
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 004102-0
PRIOR APPLICATION NUMBER: US 004284
PRIOR APPLICATION NUMBER: US 00238,897
PRIOR PILING DATE: 2000-11-09
PRIOR PILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 004335-5
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 24
SOFTHARE: PASSESQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 3289
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155074
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CRGANISM: Homo sapiens
US-09-963-285-8
      RESULT 1
US-09-963-285-8
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Sequence 1, Appli
Sequence 15, Appl
Sequence 16, Appl
Sequence 1603, A
Sequence 10475, A
Sequence 10475, A
Sequence 1141, Ap
Sequence 1141, Ap
Sequence 1151, Ap
Sequence 1513, Ap
Sequence 1513, Ap
Sequence 1513, Ap
Sequence 1677, Appl
                                                                                           March 25, 2004, 10:03:04; Search time 854.12 Seconds (without alignments) 4297.861 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/US07_FUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/Per_NEW PUB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-963-285-1

US-10-116-265-15

US-10-116-265-16

US-10-116-265-16

US-10-10-265-16

US-10-057-4818-10475

US-10-057-4818-10475

US-10-017-161-1403

US-10-017-161-1403

US-10-017-161-1857

US-10-0122-798-1187

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US-10-032-393-8
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Maximum Match 100%
Listing first 45 summaries
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CURRENT APPLICATION NUMBER: US/09/963,285
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 2E 0004102-0
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-10-10
PRIOR PLING DATE: 2000-10-10
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PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PREUSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 1.9e-241;
Matches 986; Conservative 0; Mismatches 0; Indels 1790 721 601 661 셤 ò 셤 엄 δ δ

Sequence 1, Application US/09963285
Patent No. US20020090707A1
GENERAL INFORMATION:
APPLICANT: Enerbck, Sven
APPLICANT: Rrook, Katarina
APPLICANT: Rondahl, Lena
APPLICANT: Rondahl, Lena
APPLICANT: Rondahl, Lena
TITLE OF INVENTION: PROMOTER SEQUENCES
FILE REFERENCE: 13425-042001

RESULT 2 US-09-963-285-1

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      --CCGGGGCGGCGGGTCTTAGAGCCGACGGAT 356
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                                                                                                                              1505 TCAGGCGCTCCTCGTTTTGATTGGTGCCATCCTTCTCGCAGCTGCCAGATGATTGGTGCA
                                                                                                                                                                                                            1565 AACTICCIGGAGGGGGGGGCCTGAAGAAAGIAAAACTCGCTTTGAGCCAGAAGACTT
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                                        .445 ACTIGAGCIGGGGGGGGGGAGAICIGGCIAAGAGCAICIGGGICIIAGAGCGACGGAI
                                                                                      357 ICCTGCGCTCCTCGCCCCGATTGGCGCCGGACTCCTCTAGCTGCCGGGTGALTGGCTCA
                                                                                                                                                                    AAGTTCCGGGAGGGGGGGGGCGTGGCCGAAAGTAAAACTCGCTTTCAGCAAGAAGATT
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llarity 83.2%; Pred. No. 4.6e-22;
Conservative 21; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NEW METHOD
FILE REFERENCE: 13425-10501
CURRENT APPLICATION NUMBER: 0202-04-04
PRIOR APPLICATION NUMBER: SE 010118-6
PRIOR PLILING DATE: 2001-04-05
PRIOR PLILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 15
LENGTH: 125
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US-10-116-265-15
Sequence 15, Application US/10116265
Publication No. US20030077612A1
GENERAL INFORMATION:
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      306 AGACGGAGTCGCCGCGGAGG-
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US-10-116-265-15
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Matches 104; Conservat
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1970 AGCGGGCCCGCCTGCGCTTGCCCGGGCGCGCCCTCCAGGATGCCGATCCGCCCGGTC 2029
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                                                                                                                                                                                                            CGCGCTCTCGCTCTCAGGGCCCCCCTCGCTCCCCGGCGCAGTCCGTGCGCAGGGC 960
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                                                                                2030 cecrehanecececececrecresecesaceaecenceaeceaecececese
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                                        CGCTGAAAGCGCGCCCCTGCTCGGCCCGAGCGACGACGACGCGCGCACCCTCGCCCCGG
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64.9%; Pred. No. 2.5e-63;
tive 0; Mismatches 265; Indels 5
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PACHER No. US200209707A1
GENERAL INFORMATION:
APPLICANT: Brachok, Sven
APPLICANT: Rrock, Katarina
APPLICANT: Rondahl, Lena
APPLICANT: PROMOTER SEQUENCES
FILE REFERENCE: 13425-04201
CURRENT APPLICATION NUMBER: US/09/963,285
CURRENT FILING DATE: 2001-09-05
PRIOR FILING DATE: 2000-11-09
PRIOR PLING DATE: 2000-10-10
PRIOR PLING DATE: 2000-10-10
PRIOR FILING DATE: 2000-00-26
NUMBER OF SEQ ID NOS: 24
SEQ ID NOS: 24
SEQ ID NOS: 24
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Best Local Similarity 64.9
Matches 597; Conservative
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; LOCATION: (1649)...(438)
US-09-963-285-5
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Length 805; Indels 686

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APPLICANT: Algate, Faul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Wang, Ailun
APPLICANT: Ordonez, Nadia
APPLICANT: Carter, Lauren
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
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       Score 74.2; DB 12;
Pred. No. 1.4e-08;
0; Mismatches 195;
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PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-05-14
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   7.5%;
   Query Match
Best Local Similarity 49.0
Matches 187; Conservative
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Publication No. U920040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: About Yihua
APPLICANT: About Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REPERENCE: 38-21(53223)
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 6: 285684
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921 GCCCCCCTCCCCCCCCCCGCCGCAGTCCGTGCGCGAGGGCGCCGCGGGAGCCGTCTCGGAA
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82.7%; Pred. No. 2.1e-09;
ive 13; Mismatches 0; Indels
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OTHER INFORMATION: unsure at all n locations
FEATURE:
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Sequence 16, Application US/10116265
Publication No. US20030077612A1
GENERAL INFORMATION:
APPLICANT: Ekblom, Jonas
TITLE OF INVENTION: NEW METHOD
FILE REPRENCE: 13425-105001
CURRENT APPLICATION NUMBER: US/10/116,265
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: SE 010218-6
PRIOR PILING DATE: 2001-04-05
PRIOR PILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,384
FRIOR APPLICATION NUMBER: 60/281,384
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FRSENSEQ FOR WINGOWS Version 4.0
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52; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 75
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Best Local S
Matches 62
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Remaining Prior Application data removed - See File Wrapper or PALM.

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17943 CGGGGGCCCCCCCGGCCCGGCCCGGCCCGCGNGCCGGCCCCGCCCCGCCCGCCCGGC
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PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR PLING DATE: 2000-08-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 11290
SOFTWARE: PASISEQ for Windows Version 3.0
SEQ ID NO 10475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 51657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18180 Grecescectriccectrrececerrecestrices 18222
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APPLICANT: SANT, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
CURRENT FILING DATE: 084335/0152
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US 2001/246789
PRIOR APPLICATION NUMBER: US 2001/246789
PRIOR PILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 1403
LENGTH: 1117
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48.9%; Pred. No. 2.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | PEATURE:
| NAME/KEY: misc feature
| LOCATION: (1)...(51657)
| OTHER INFORMATION: n = g, a, c or
| US-10-154-884B-10475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 48.9
Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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US-10-017-161-1403/c
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APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-01352103
CURRENT FILING DATE: 2000-05-23
PRIOR PLILOR DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200, 303
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PLILOR PREDICATION NUMBER: US 60/200, 999
PRIOR PLILOR DATE: 2000-05-01
PRIOR PRIOR PPLICATION NUMBER: US 60/200, 999
PRIOR PRIOR PPLICATION NUMBER: US 60/200, 999
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Pred. No. 2.2e-07;
0; Mismatches 203; Indels
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NUMBER OF SEQ ID NOS: 10979
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10475
LENGTH: 51657
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                                                                                                                                                                                                                                                         ) NAME/KEY: misc_feature

) LOCATION: (1)...(51657)

) OTHER INFORMATION: n = g, a, c or

US-10-057-475B-10475
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Matches 197; Conservative
                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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US-10-154-884B-10475
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Best Local
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FEATURE:
NAME/KEY: modified base
LOCATION: (351)
OTHER INFORMATION: a, t, c, g, unknown or other
NAME/KEY: modified base
LOCATION: (360)..(361)
OTHER INFORMATION: a, t, c, g, unknown or other
OTHER INFORMATION: (360)..(361)
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LOCATION: (405)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
LOCATION: (431)..(432)
OTHER INFORMATION: a, t, c, g, unknown or other
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DTHER INFORMATION: a, t, c, g, unknown or other FRATURE:
FREATURE:
FOREX. modified base
LOCATION: (398)...(399)
DTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (173)

THER INFORMATION: a, t, c, g, unknown or other
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TTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: modified base.
LOCATION: (343)...(344)
DTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (440)...(444)
CTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (464)..(465)
OTHER INFORMATION: a, t, c, g, unknown or other
PERTURE:
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LOCATION: (378)
THER INFORMATION: a, t, c, g, unknown or other
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OCATION: (401)...(402)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (434)
OTHER_INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                               LOCATION: (170)
OTHER INFORMATION: a, t,
                                                                                                          NAME/KEY: CDS
LOCATION: (201)..(917)
FEATURE:
NAME/KEY: modified_base
ORGANISM: Homo sapiens
                                               source
(1)..(1117)
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DOCATION: (468)

NAME/KEY: MEGGIFIED ASSESSMENTION: a, t, c, g, unknown or other PRATURE:
NAME/KEY: medgified base

OTHER INFORMATION: a, t, c, g, unknown or other PRATURE:
NAME/KEY: medgified base

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Sequence 1141, Application US/10292798
Publication No. US20030235833A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAMES/KET: modified base LOCATION: (173) ..(173) ..(173) ...(173) ...(173) ...(173) ...(173) ...(173)
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LOCATION: (351)...(356)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (360)..(361)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (378)..(378)
OTHER INFORMATION: a, t, c, g, unknown or other
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                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: Patentin Ver: 2.1
LENGTH: 1117
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LOCATION: (343)..(344)
OTHER INFORMATION: a, t, c,
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OTHER INFORMATION: a, t, c,
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NAME/KEY: modified base
COCATION: (170)..(170)
OTHER INFORMATION: a, t, c
FEATURE:
NAME/KEY: modified base
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LOCATION: (207)..(306)
OTHER INFORMATION: a, t,
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LOCATION: (380)..(383)
OTHER INFORMATION: a, t,
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LOCATION: (398)..(399)
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FEATURE:
LOCATION: (1)..(1117)
FEATURE:
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(201)..(917)
                                      RESULT 10
JS-10-292-798-1141/c
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LOCATION:
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7.4%; Score 73; DB 14; Length 1117;
Best Local Similarity 36.0%; Pred. No. 3.3e-08;
Matches 157; Conservative 0; Mismatches 279; Indels
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LOCATION: (673)..(675)
OTHER INFORMATION: a, t, c, g, unknown or other
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                         NAME/KEY: modified_base
LOCATION: (650)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (694)..(696)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                  g, unknown or other
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LOCATION: (652)..(653)
OTHER INFORMATION: a, t, c,
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NAME/KEY: modified_base
LOCATION: (688)..(689)
OTHER INFORMATION: a, t, c,
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                                                        NAME/KEY: modified_base
LOCATION: (646)
OTHER INFORMATION: a, t,
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THER INFORMATION: a, t,
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LOCATION: (648)
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LOCATION: (698)
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NAME/KEY: modified base

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NAME/KEY: modified base
LOCATION: (431)...(432)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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DTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (434)...(434)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (468)..(468)
OTHER INFORMATION: a, t, c, g, unknown or other
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DTHER INFORMATION: a, t, c, g, unknown or other
                                                     g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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OCATION: (487)...(497)
WHER INFORMATION: a, t, c, g, unknown or other
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CCATION: (509)...(510)
THER INFORMATION: a, t, c, g, unknown or other
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OCATION: (525)...(527)
THER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (557)..(561)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
CHCATION: (565). (565)
CHERR INFORMATION: a, t, c, g, unknown or other
FEATURE:
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LOCATION: (539)...(542)
JTHER INFORMATION: a, t, c, g, unknown or other
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THER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (552)...(552)
DIHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t,
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798 INTCCCCCCCCCNINCONNICON SECULACION CONTROL CONTROL
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7.4%; Score 73; DB 15; Length 1117;
Best Local Similarity 36.0%; Pred. No. 3.3e-08;
Matches 157; Conservative 0; Mismatches 279; Indels
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NAME/KEY: modified base
LOCATION: (689). (689)
OTHER INFORMATION: a, t, c, g, unknown or other
FRATURE:
NAME/KEY: modified base
LOCATION: (694). (696)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (629)..(629)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (646)..(646)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, L, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (615)..(615)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (617)...(617)
PEATURE INFORMATION: a, t, c, g, unknown or other
PEATURE:
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LOCATION: (619)..(622)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
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NAME/KEY: modified base
LOCATION: (648)..(648)
FEATURE INFORMATION: a, t, c, g, unknown or other
FEATURE:
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NAME/KES: modified base
NAME/KES: modified base
OCHEN: (669)...(669)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                         g, unknown or other
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                                                                                                                                                                                                                                                                                                               PEATURE:
NAME/KEY: modified base
LOCATION: (605)..(610)
PEATURE: INFORMATION: a, t, c, g
                                                                  FEATURE:
NAME/KEY: modified_base
LOCATION: (588)..(588)
OTHER INFORMATION: a, t, c,
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NAME/KEY: modified base
LOCATION: (1105)..[1107)
OTHER_INFORMATION: a, t, c, g, unknown or other
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CCCTION: (1130)
CTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
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LOCATION: (1066)...(1067)
OTHER INFORMATION: a, t, c, g
FEATURE:
NAME/KEY: modified base
LOCATION: (1082)...[1084)
OTHER INFORMATION: a, t, c, g
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LOCATION: (995)
OTHER INFORMATION: a, t, c,
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LOCATION: (754)...(756)
OTHER INFORMATION: a, t, c,
FEATURE: NAME/KEY: modified_base
LOCATION: (761)
OTHER INFORMATION: a, t, c,
FEATURE:
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LOCATION: (920)
OTHER INFORMATION: a, t, c,
PEATURE:
NAME/KEY: modified_base
LOCATION: (941)
OTHER INFORMATION: a, t, c,
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LOCATION: (897)
OTHER INFORMATION: a, t, FEATURE:
    NAME/KEY: modified base CCATION: (745)..(747)
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LOCATION: (763)
OTHER INFORMATION: a, t,
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LOCATION: (843)
OTHER INFORMATION: a, t,
                                                             FEATURE:
NAME/KEY: modified base
LOCATION: (750)
OTHER INFORMATION: a, t,
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LOCATION: (818)
OTHER INFORMATION: a, t,
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LOCATION: (752)
OTHER INFORMATION: a, t,
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THER INFORMATION: a, t,
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NAME/KEY: modified_base
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NAME/KEY: modified_base
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                                     901 GGCGCTCTCTCGCTCTCAGGGCCCCCTCGCTCCCCGGCCGCAGTCCGTGCGCGAAGGC 960
                                                                                                                                                                                                                                                                                      721 AGCGGGGCGGCGCTGCGCTTGCCCGGGGCGCGCCCTCCAGGATGCCGATCCGCCCGGTC 780
                                                                               781 COCTGAAAGCGCGCCCCTGCTCGGCCCGAACGACGCACCGCGCACCTCGCCCCGG
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Sequence 1857, Application US/10017161

Publication No. US20030143668A1

GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, WITHARA

TILLEOF INVENTANI, HIROYUKI

TILLEOF INVENTANI, HIROYUKI

TILLEOF INVENTANI, NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFREENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161

CURRENT APPLICATION NUMBER: US/267161

CURRENT APPLICATION NUMBER: JP 2001/246789

PRIOR FILING DATE: 2001-06-18

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2430

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1857

TADEOF LENGTH: 3163

TADEOF LENGTH: 3163
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NAME/KEY: source
LOCATION: (1)..(3163)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(2963)
FEATURE:
NAME/KEY: modified base
LOCATION: (556)..(655)
OTHER INFORMATION: a, t, c, g, unknown or other
NAME/KEY: modified base
LOCATION: (658)..(669)
OTHER INFORMATION: a, t, c, g, unknown or other
DOCATION: (658)..(669)
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NAME/KEY: modified base
LOCATION: (671)..697)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (709)..(736)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (739)..(743)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (704)..(707)
OTHER INFORMATION: a, t, c,
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US-10-017-161-1857/c
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FEATURE:
NAME/KEY: modified base
LOCATION: (1247)..[1248)
OTHER INFORMATION: a, t, c, g, unknown or other
                                g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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              LOCATION: (1147)
OTHER INFORMATION: a, t, c,
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LOCATION: (1674)
OTHER INFORMATION: a, t, c,
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NAME/KEY: modified base
LOCATION: (1866).. [1965)
OTHER INFORMATION: a, t, c,
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NAME/KEY: modified_base
LOCATION: (1162)
OTHER INFORMATION: a, t, c
FEATURE:
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LOCATION: (1202)
OTHER INFORMATION: a, t,
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OCATION: (1635)
THER INFORMATION: a, t,
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OCATION: (1544)
THER INFORMATION: a, t,
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OCATION: (1601)
WHER INFORMATION: a, t,
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CCATION: (1605)
THER INFORMATION: a, t,
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LOCATION: (1637)
OTHER INFORMATION: a, t,
FEATURE:
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LOCATION: (1852)
OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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LOCATION: (1500)
THER INFORMATION: a, t,
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THER INFORMATION: a, t,
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NAME/KEY: modified_base
TOCATION: (1695)
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NAME/KEY: modified_base
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APPLICANT: SUWA, MAKIKO
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI KIYOSHI
APPLICANT: AKAI KIYOSHI
APPLICANT: AKAI KIYOSHI
APPLICANT: AKIVAA, YUTAKA
APPLICANT: ALUARANA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENITON: GUAJSE/166
CURRENT APPLICATION NUMBER: 10/017,161
FRICA FILING DATE: 2002-11-13
FRICA FILING DATE: 2001-12-18
FRICA FILING DATE: 2001-12-18
FRICA FILING DATE: 2001-06-18
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Pred. No. 5.7e-07;
0; Mismatches 191; Indels 0;
LOCATION: (1968)..(1980)
OTHER INFORMATION: a, t, c, g, unknown or other FEATURES: modified base
LOCATION: (1982)..(2009)
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NOAMING modified base
NOAMING (658). (669)
OTHER INFORMATION: a, t, c, g, unknown or other
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Best Local Similarity 45.7%;
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: modified base
LOCATION: (556)..(655)
OTHER INFORMATION: a, t, c,
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LOCATION: (201)..(2963)
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NAME/KEY: modified base
LOCATION: (671)..(697)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (739)..(743)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
OCATION: (995)...(995)
TYPHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (704)..(707)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (709)..(736)
OTHER_INFORMATION: a, t, c, g, unknown or other
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LOCATION: (745)..(747)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
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OTHER INFORMATION: a, t, c, g, unknown or other
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OCATION: (897)...(897)

OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY:
NAME/KEY:
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(941)..($941)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
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(993)..($93)
OTHER INFORMATION: a, t, c, g, unknown or other
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COCATION: (752). (752)
THER INFORMATION: a, t, c, g, unknown or other
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NAME/REY: modified base
MACATION: (818)..(818)
MINER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (892)...(892)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
COCATION: (920)...(920)
THER INFORMATION: a, t, c, g, unknown or other
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COCATION: (761)..(761)
THER INFORMATION: a, t,
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PARE/UKE:
PRAIUKE:
PAME/KEY: modified base
LOCATION: (1147)...(1147)
FEATURE:
NAME/KEY: modified base
LOCATION: (1162)...(1162)
CUTER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (1202)...(1202)...(1202)
CUTER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (1233)...(1233)
CTHER INFORMATION: a, t, c, g, unknown or other
PEATURE:
NAME/KEY: modified base
LOCATION: (1233)...(1233)
CTHER INFORMATION: a, t, c, g, unknown or other
NAME/KEY: modified base
LOCATION: (1247)...(1248)
PEATURE:
NAME/KEY: modified base
LOCATION: (1247)...(1248)
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LOCATION: (1261)...(1261)
OTHER INFORMATION: a, t, c, g, unknown or other
PEATURE:
NAME/KEY: modified base
LOCATION: (1485)...(1485)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (1500)...(1500)
OTHER INFORMATION: a, t, c, g, unknown or other
NAME/KEY: modified base
LOCATION: (1544)...(1544)
OTHER INFORMATION: a, t, c, g, unknown or other
PEATURE:
NAME/KEY: modified base
LOCATION: (1544)...(1544)
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NAME/KEY: modified base
LOCATION: (1601)...(1601)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (1605)...(1605)
OTHER INFORMATION: a, t, c, g, unknown or other
NAME/KEY: modified base
LOCATION: (1605)...(1605)
OTHER INFORMATION: a, t, c, g, unknown or other
OCATION: (1605)...(1635)
OTHER INFORMATION: a, t, c, g, unknown or other
OCATION: (1605)...(1635)
NAME/KEY: modified base
LOCATION: (1066)..[1067)
FEREN INFORMATION: a, t, c, g, unknown or other
FEATURE:
                                                                                                                                                                                                                       NAME/KEY: modified base
LOCATION: (1105)..[1107)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (1130)...[1130)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (1637)...[1637)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (1082)...(1084)
OTHER INFORMATION: a, t,
FEATURE:
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NAME/KEY: modified_base
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APPLICANT: Haselbox, Robert
APPLICANT: Haselbox, Robert
APPLICANT: Wall, Daniel
APPLICANT: Gross, Molly
TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REPERENCE: ELITRA, 010A
CURRENT PILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 05/259,434
PRIOR APPLICATION NUMBER: 05/259,434
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-10-66
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 68
SOTWWARE: RESURE OF CT Windows Version 4.0
                                                                                                                                                                                                                                            Indels
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llarity 48.4%; Pred. No. 4.2e-06;
Conservative 0; Mismatches 198;
                                                                                                                      6.8%; Score 67.4; DB 12; 47.1%; Pred. No. 7.3e-07;
                                                                                                                                                                                                                                            0; Mismatches 184;
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Publication No. US20030027286A1
GENERAL INFORMATION:
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US-10-032-393-47
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                                                                                                                      Query Match
Best Local Similarity 47.1
Matches 164; Conservative
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            US-10-424-599-107958
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US-10-032-393-47/c
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US-10-424-599-107958/C
iSequence 107958, Application US/10424599
i Sequence 107958, Application US/10424599
i Publication No. US20040031072A1
i GENERAL INFORMATION:
i APPLICANT: La Rosa Thomas J
i APPLICANT: La Rosa Thomas J
i APPLICANT: Cavoulic David K
i APPLICANT: Zhou Yihua
i APPLICANT: Cavoulic David K
i APPLICANT: Cavoulic David K
i APPLICANT: Cavoulic David K
i TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
i TITLE OF INVENTION: 18-1202
i TITLE OF INVENTION: 18-1202
i CURRENT APPLICATION NUMBER: US/10/424,599
i CURRENT FILING DATE: 2003-04-28
i SEQ ID NO 107958
i LENGTH: 771
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LOCATION: (1)..(771)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_68501C.1
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NAME/KEY: modified base
LOCATION: (1968)...[1980)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                    or other
                                                                                                                                                                 NAME/KEY: modified_base
COCATION: (1695)..(1695)
COTHER INFORMATION: a, t, c, g, unknown or FEATURE:
NAME/KEY: modified_base
LOCATION: (1852)..(1852)
OTHER INFORMATION: a, t, c, g, unknown or content of the content o
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LOCATION: (1866)..(1965)
OTHER INFORMATION: a, t, c, g, unknown
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Best Local Similarity 45.7%;
Matches 161; Conservative
LOCATION: (1674)...(1674)
OTHER INFORMATION: a, t,
FEATURE:
NAME/KEY: modified_base
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Sequence 8, Application US/10032393
Fublication No. US20030027286A1
SAPELCANT: Haselbeck, Robert
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Gross, Molty
ITILE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USS
TILE REFERENCE: ELITRA.010A
CURRENT APPLICATION NUMBER: US/10/032,393
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/259,434
PRIOR APPLICATION NUMBER: 60/259,434
PRIOR PILING DATE: 2001-09-06
PRIOR PILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 12739
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932 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACK14809 of RPCT-98 library from Drosophila melanogaster (fruit
AL066742
AL066742.1 GI:4945205
CG756569 PO51-4-B0
CC210735 CH261-185
BX415926 BX415926
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Submitted (12-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr.)
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Droscophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Droscophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Droscophila melanogaster BAC library was prepared by Kazutcoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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CG757066 P052-2-A0
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                                                                                 March 25, 2004, 09:53:09; Search time 7451.24 Seconds (without alignments) 3951.570 Million cell updates/sec
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             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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(bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/clone lib="Ppa EcoRI BAC Library"
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                                                                                      Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 04477071601371
Eax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
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Pristionchus pacificus
Pristionchus pacificus
Bukaryota, Metazoa; Nematoda, Chromadorea, Diplogasterida,
Bukaryota, Metazoa; Nematoda, Chromadorea, Diplogasterida,
1 (bases 1 to 1628)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)
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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BRT14B09"
/clone lib="RRCI-98"
/note="end : T7"
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Apports sequence.
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/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 72"
/note="Corgan: Skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArCC/DcTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLAM12332 row; l column: 22
High quality sequence stop: 294.
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                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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52.0%; Pred. No. 1.9e-06;
tive 0; Mismatches 198;
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/db_xref="taxon:9606"
/clone="IMAGE:5578149"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="cSoD1080vB07"
/clone_Tib="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tist strand cDNA was primed with a NotI-oligo(dT)
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                Enail: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4309.f For
nuce information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?eeq=CsObIO80CCG4NP1ccluster=4309.f. Contact :
Feng Liang Email : fliang@lifetch.com UNL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBIO80CCG4NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  760 AGGATGCCGATCCGCCCGGTCCGCTGAAAGCGCGCGCCCCTGCTCGGCCCCGAGGACGAC
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44.0%; Pred. No. 1.2e-06;
tive 57; Mismatches 202; Indels 2;
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    191 91006 EVRY cedex - France
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/mol_type="genomic_DNA"
/strain="Red_Jungle_Fowl"
/db_xref="taxon:9031"
/clone="CH261-185P7"
                                                                                                                                                                                                                                                                                                                      1. .1159
/organism="Gallus gallus"
                                                                                                                                                                         Contact: Richard K. Wilson
 GI:30529403
                            Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                               /sex="female"
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CC261-185P7 Sp6.2 CH261 Gallus gallus genomic clone CH261-185P7,
genomic survey sequence.
CC210735
                               1 (bases 1 to 1406)
Stintyasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An inteagrated physical and genetic map of the nematode Pristionchus
pacificus
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/mol_type="genomic DNA"
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/db_xref="taxon:54126"
/clone lib="pa EcoRI BAC Library"
/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."
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   Chromadorea; Diplogasterida;
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Pred. No. 2.7e-06;
0; Mismatches 231; Indels 0;
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                                                                                                                                                              Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tal: 00497071601371
                                                                                               Mol. Genet. Genomics 269 (5), 715-722 (2003)
22835951
                                                                                                                                                                                                                                   Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
 Eukaryota, Metazoa, Nematoda, Chi
Neodiplogasteridae, Pristionchus
                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           9.6%;
ilarity 49.8%;
Conservative
                                                                                                                                               Contact: Sommer RJ
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Best Local Similarity
Matches 229; Conserv
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/note="Vector: pTARBAC2.1; Site_l: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - For library and clone
ordering information: http://www.chori.org/bacpac"
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae, Gallus.

1 (bases 1 to 1159)

Rremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

Gallus gallus BAC End Reads
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: Sp6 ATTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 71
High quality sequence stop: 159.
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9.5%; Score 93.2; DB 28;
Best Local Similarity 51.3%; Pred. No. 4.6e-06;
Matches 235; Conservative 0; Mismatches 222;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Primates, Catarrhini, Hominidae, Homo.
El (Dases I to 1046)
In 10 1046)
In NH-MGC http://mgc.nci.nih.gov/
Lu Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Biosciance Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2603 row'
High quality sequence stop: 206.
High quality sequence stop: 206.
                                                                                                                                                                                                                       1046 bp mRNA linear EST 21-AUG-2002
AGENCOURT 8863775 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6423858
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    1046
    organism="Homo sapiens"

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Genoscope - Centra National de Sequencage
Genoscope - Centra National de Sequencage
Brail: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9016.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq-CSSCAP008CD01QP1&cluster=9016.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://tullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP008CD01QP1.
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/clone lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
/incte="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(H) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned
the Not I and BCORV sites of the pCMVSPORT 6 vector.
                                                                                                                                         BX415926 1144 bp mRNA linear EST 13-MAY-2003
84115926 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAPO08YH01
5-PRIME, mRNA sequence.
BX415926
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Catarrhini; Hominidae; Homo.
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9.4%; Score 93; DB 13; Length 1144;
Best Local Similarity 39.4%; Pred. No. 5e-06;
Matches 162; Conservative 76; Mismatches 172; Indels
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Library was not normalized."
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/db_xref="taxon:9606"
/clone="CSOCAP008YH01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata,
Mammalia, Butheria, Primates,
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BX415926/c
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Lotoki, Y., Hattozi, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Matanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEM), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mall:chimpessagsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170
Was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-NOV-2001
                                                                                            831 CTCGCCCCGGAGGCTGCCAGGAGACCGGGGCCGCCCTCCCCGCTCCCCTCCTCTCCCCTT 890
                                                                                                                                                                                                                                                                                                                          AG128304 1023 bp DNA linear GSS 04-NOV-200 bp. troglodytes DNA, clone: PTB-139G20.R, genomic survey sequence. AG128304.1 GI:16657469
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Buha troglodytes
Bukaryots, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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48.1%; Pred. No. 8.1e-06;
tive 0; Mismatches 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .1023
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db xref="taxon:9598"
/clone="PTB-139G20.R"
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R.Site 1 : SacI
R.Site 2 : SacI.
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1016 bp mRNA linear EST 20-AUG-2002 AGENCOURT 8885548 NCI CGAP Co24 Mus musculus cDNA clone IMAGE:6397594 5', mRNA sequence.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.go.
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAM18895 row: 1 column: 11
High quality sequence stop: 407.

Location/Qualifiers

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// Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 1016)
NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xxxe=rvoxn:10090"
/clone="INAGE:6397594"
/lab_host="DH10B (Ti phage-resistant)"
/clone=lib="NCI CGAP Co24"
/note="Organ: colon, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
    CTCGGCCCGAGCGACGACGCGCGCACCTCGCCCCGGAGGCTGCCAGGAGACCGGGGC
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/strain="FVB/N"
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AGENICOURT 6597561 NIH_MGC_41 Homo saplens cDNA clone IMAGE:5480748 5', mRNA Sequence. BM562099 1 GI:18807897 8ST.
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/lab host="DH108 (phage-resistant)"
/clone_lib="NIH MGC_41"
/clone_lib="NIH MGC_41"
/note="Organ: SKin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECR1; CDNA made by oligo-dT priming. Directionally cloned
into BcoR1/KhoI sites using the following 5 adaptor:
GGCAGGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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                                                                                                                                               573 CCCCCGSSCCCCSSCGSSSCSCSSSSSSCGCSSCSCSCCCCSSSSCSCSSSSS 514
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2004 row: b column: 13
High quality sequence stop: 206.
High quality sequence stop: 206.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        393 CCGCCCCSSCCCTCCCCCCCGCGCCCCCCCGS 360
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5480748"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Homo sapiens
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BX349688
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TCCTGGAGCCAGCGAGGAGGAGCGGGCGGCGCTGCGCTTGCCCCGGGGCGCGCCCTCCAGGA 763
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand oDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand oDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.ons.fr, www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7092.r For
more information about this cluster, see
http://www.genoscope.ons.fr/
cgi-bin/cluster.cgi?seq=CSOBAH015ZB03NP1&cluster=7092.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAH015ZB03NP1.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Frull-length cDNA libraries and normalization
Unpublished (2001)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI062YK05"
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Inote="Site 1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [6]
sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Submission, Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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                                                                                                                                                                                                                                                                                                                                        Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'clone_lib="RIKEN full-length enriched, 10 day neonate
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/lab_host="DH10B"
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1. .716
/organism="Mus musculus"
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clone="4732425M02"
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/strain="C57BL/6J"
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Matches 247; Conservative
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Mus musculus (bouse mouse)

Mus musculus (broadata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Matheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

I (bases I to 716)

S Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,

Hara,A., Hiramoto,K., Hori,P., Ishini,Y., Ito,M., Kawai,J.,

Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,

Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sano,H., Sasaki,D., Shibata,K., Shihata,K., Shiha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB612862 RIKEN full-length enriched, 10 day neonate skin Mus musculus cDNA clone 4732425M02 5', mRNA sequence.
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
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KEYWORDS
SOURCE
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- Web: www.genoscope.cns.fr

- Web: www.genoscope.cns.fr

- Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see http://www.fruitily.org The BDGP Drosophila

melanogaster BAC library was prepared by Kazutcyo Gosegawa and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

BCORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain v2: on bw sp, the same strain used for the BDGP's

and how to order individual BAC clones, the entire library or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNS0072Q 132 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTGCCGATTCGCTGGGGGCTTGGAGAGCCTCCTGCGCCCTCCTCGCGCCGAGG 627
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452 recserssbeyekekekekedeekeerkeerkeekeedekeeekeedegeegegegegeneere 511
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                                                                                                                                                                                                                                                                              508 TGGCCTCTTTTTCTGGGCTCAGCGGGGGGCAGCCGCTCGGACCCCGGGCGCGCCTCGG
                                     GICCGCIGAAAGCGCGCCCCTGCTCGGCCCCGAGGACGACGACGCGCGCACCCTCGCCC
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neopiera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Genoscope.
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/mol_type="genomic DNA"
/db_xref="taxon.7227"
/clone="BACR14809"
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/note="end : T7"
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/_clone_lib="Homo saplens PLACENTA"
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with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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BX464554 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE007YB11
3-PRIME, mRNA sequence.
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Catarrhini, Hominidae, Homo.
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cgi-bin/cluster.cgi?seq=cSlDE002ZF03NPiscluster=3370.r. Contact : Sequence of Sequ
                                                                                     838 CGGAGGCTGCCAGGAGACCGGGCCGCCCCCTCCCCCTCCCCCTCTCCCCCTCTGGCTC
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larity 38.8%; Pred. No. 1.5e-05;
Conservative 70; Mismatches 200; Indels 0.
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Mammalia; Butheria; Primates; Catarrhini; Hor
1 (bases 1 to 807)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE007YB11"
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Search completed: March 25, 2004, 15:29:54 Job time : 7456.24 secs

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March 25, 2004, 07:40:23 ; Search time 12.4532 Seconds (without alignments) 4093.601 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Abv43572 Human pro Abg57116 Human col Ac£6994 Photochab Ac£68904 Photochab Ac\$6663 EST clone Ac\$0439 C. glutam Abv4835 Human bro Abc10067 Human bro Abc1007 Human bro Ac\$6407 Human pol Ac\$6407	INTS			16 for detecting SNP TSC0057728.	human; diagnosis; PNA; cancer; CNS; lation; cardiovascular; primer; Ss; lnal; respiratory; immune; metabolic.								on co	equence Listing; German.	describes novel oligonucleotide primers or peptide nucleic gomers for detecting single nucleotide polymorphisms (SNP) ethylation status in chemically pretreated genomic DNA. The les are used for diagnosis and/or prognosis of cancer and a ses including immune system, gastrointestinal, respiratory, as system, cardiovascular and metabolic disorders. The also used for detecting cell type differentiation. ABCO010 00010-ABE99998, ABHO0010-ABH99989 and ABI00010-ABE99989, and coligomers described in the invention. NOTE: The sequence patent did not form part of the printed specification, but
ABV43572 ABC59116 ACF68904 ACF68904 ACA00439 ACA00439 AB148358 AB148358 AB11183 ABA11183 ABA11183 ABA182599 AB18359 AB163559	ALIGNMENTS			NO 369586	phism; methyJ intesti						п К;		for dotide	9pp + geg	oligon tting sli is in ch diagnos mmune sy vascula recting ABH0001 Libed in
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EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;

cross-species comparison

JS2003104410-A1

05-JUN-2003

Homo sapiens.

Human microarray DNA oligonucleotide SEQ ID NO 123886

14-0CT-2003

ACK23905;

ВР.

ACK23905 standard; DNA; 25

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a PCR primer for the amplification of sefB from Salmonella enteritidis. The nucleic acid produced can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                              Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody; polymerase chain reaction; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 12; DB 2; Length 19; 100.0%; Pred. No. 8.7e+03;
                                                                             Length 12;
                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 BP; 4 A; 3 C; 2 G; 10 T; 0 U; 0 Other;
                                             Sequence 12 BP; 1 A; 3 C; 0 G; 8 T; 0 U; 0 Other;
                                                                          100.0%; Score 12; DB 5; I 100.0%; Pred. No. 8.7e+03;
was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis sefB PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 11; Col 51; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Doran JL
                                                                                                                                                                                                                                                 AAT74184 standard; DNA; 19 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-00054452
                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                            Local Similarity 100, ses 12; Conservative
                                                                                                                                        1 GGAAAGTAAAAA 12
                                                                                                                                                                       12 GGAAGTAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collinson SK, Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-309886/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-APR-1993;
                                                                                                                                                                                                                                                                                                            25-MAR-2003
29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5635617-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-NUT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                AAT74184;
                                                                               Query Match
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Matches
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New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

16-MAR-2001; 2001US-0276759P 15-MAR-2002; 2002US-00098263

(AFFY-) AFFYMETRIX INC.

WPI; 2003-567953/53

dittmann MP;

Claim 1; SEQ ID NO 123886; 9pp; English.

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in manipais of genetic variation or in hybridisation to a DNA library, or in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring can expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes in situ hybridisation, in Southern, Northern or dotonce the hybridisation to identify or detect the sequence or specific or additional subclones containing segments of many members of any sequenced. The sequence or specific cold the previously sequenced. The sequence presented is one of the containing cold in electronic format directly contained for this patent can also be obtained in electronic format directly contains the microarray. Note: The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25 BP; 4 A; 8 C; 4 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV26241 standard; DNA; 28 BP.
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Best Local Similarity
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AAV26241/c
ID AAV26
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Gaps

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0; Indels

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12; Conservative 1 GGAAAGTAAAAA 12

Matches

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14 GGAAAGTAAAA

RESULT 3 ACK23905/c

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pseudorabies virus; feline immunodeficiency virus; FIV; heartworm;
                                                                                                                                                                                                                                    WPI; 1998-130677/12.
                                                                                                                                                                                 SYTR ) SYNTRO CORP.
                                                                                                                                                         25-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9957295-Al
                                                                              409804684-A1
                                                                                                                               25-JUL-1997;
                                                                                                                                                                                                            Cochran MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2000
                                                                                                       05-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ34901;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a PCR primer from the present invention.

The present invention specifically describes recombinant swinepox virus

C (SPV) comprising a foreign DNA (I) inserted into a SPV genome which is

c capable of being expressed in a host cell into which the virus is

c capable of being expressed in a host cell into which the virus is

c corresponding to a 3.2 kb subfragment of the HindlII K fragment which

c corresponding to a 3.2 kb subfragment of the WindlII K fragment which

c contains both a HindlII and an BCORI site, of the SPV genome, and

c optionally (b) an AccI site within a region corresponding to a 3.6 kb

thindlII to BgIII subfragment of the HindlII M fragment. The recombinant

SPV can be used in a vaccine for immunising an animal against SPV. The

invention also provides a method for testing a swine to determine whether

the swine has been vaccineed with the vaccine, particularly containing S

c SPV-008, or is infected with a naturally occurring wild-type

c sendorabies virus. Also (I) inserted into recombinant SPV can be used in

d diagnostic assay, e.g. Feline immunodeficiency virus (FTV) env and gag

c maninodeficiency caused by FIV and to detect feline

immunodeficiency caused by FIV and to detect feline

immunodeficiency caused by FIV and to detect feline

immunits respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                   Recombinant swine pox virus - useful in vaccine for immunising animal against swine pox virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Swinepox virus; SPV; recombinant; vaccine; immunisation; diagnosis;
                                                                              Swinepox virus; SPV; recombinant; vaccine; immunisation; diagnosis; pseudorabies virus; feline immunodeficiency virus; FIV; heartworm; Dirofilaria immitis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIV gag-protease gene PCR primer from WO9804684 Example 44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 12; DB 2; Length 28; 100.0%; Pred. No. 8.7e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28 BP; 4 A; 9 C; 4 G; 11 T; 0 U; 0 Other;
                                                        FIV gag gene PCR primer from WO9804684
                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 76; 473pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV26158 standard; DNA; 28 BP
                                                                                                                                              Feline immunodeficiency virus
                                                                                                                                                                                                                           97WO-US012212.
                                                                                                                                                                                                                                                    96US-00686968.
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Guery Match
Best Local Similarity lov...
Best Local 12; Conservative
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                               24-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGAAAGTAAAA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 GGAAGTAAAA 16
                                                                                                                                                                                                                                                                                                       Cochran MD, Junker DE;
                                                                                                                                                                                                                                                                                                                              WPI; 1998-130677/12.
                                                                                                                                                                                                                                                                             (SYTR ) SYNTRO CORP.
                                                                                                                                                                          WO9804684-A1
                                                                                                                                                                                                                           25-JUL-1997;
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                                                                                                                                                                                                   05-FEB-1998
                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV26158;
        AAV26241;
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The present sequence represents a PCR primer used in an example from the present invention. The present invention specifically describes recombinant swinepox virus (SPV) comprising a foreign DNA (I) inserted into a SPV genome which is capable of being expressed in a host cell into which the virus is introduced, where (I) is inserted into: (a) an ECORI site within a region corresponding to a 3.2 kb subfragment of the HindIII R fragment which contains both a HindIII and an ECORI site, of the SPV genome, and optionally (b) an AcI site within a region corresponding to a 3.6 kb HindIII to BglII subfragment of the HindIII M fragment. The recombinant SPV can be used in a vaccine for immunising an animal against SPV. The invention also provides a method for testing a swine to determine whether the swine has been vaccinated with the vaccine, particularly containing S-SPV-008, or is infected with a naturally occurring wild-type pseudorables virus. Also (I) inserted into recombinant SPV can be used in a diagnostic assay, es. 9. Feline immunodeficiency virus (FIV) env and gag genes and Dirofilaria immitis is and to detect heartworm caused by D. immitis respectively caused by FIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant swine pox virus - useful in vaccine for immunising animal against swine pox virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 12; DB 2; Length 28; 100.0%; Pred. No. 8.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 28 BP; 4 A; 9 C; 4 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIV gag/protase gene PCR primer 11/94.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 44; Page 214; 473pp; English.
Dirofilaria immitis; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
AAZ34901/c
ID AAZ34901 standard; DNA; 28 BP.
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                                                                                                                    Feline immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-00686968.
                                                                                                                                                                                                                                                                                                                                                     97WO-US012212.
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nes 12; Conservative
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The present invention relates to a recombinant virus comprising at least one foreign nucleic acid encoding a protein selected from feline cytotoxic I lymphocyte accessory molecules CD28, CD36, CD36 or CTA-4, which is capable of expression when the virus is introduced into an appropriate host. The virus can be administered to the feline in order to immunodeficiency disease, feline leukemia, feline in response to prevent or treat feline in order to cancers, degenerative and autoimmune diseases and immunodeficiency. The present sequence is a PCR primer described in the exemplification of the invention. (Updated on 07-AUG-2003 to correct OS field.) (Updated on 29-AUG-2003 to stended on 29-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoletin; apoptosis related brotein; cadherin; coylin; polymerse; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection;
                                                           New recombinant virus, useful for immunizing felines to prevent or tree
feline immunodeficiency virus, comprises foreign nucleic acid encoding
feline cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 12; DB 6; Length 28; 100.0%; Pred. No. 8.7e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28 BP; 4 A; 9 C; 4 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                      Disclosure; Page 61; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human SNP oligonucleotide #3426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAL30218 standard; DNA; 48 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-DEC-2000; 2000WO-US035498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-DEC-1999; 99US-0173419P.
27-DEC-2000; 2000US-00173419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nervous system disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
ses 12; Conservative
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                     WPI; 2002-415200/44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                CTLA-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL30218/
ID AAL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                            This oligonuclectide represents downstream primer 11/94.10 that was used in the PCR amplification of the FIV gag/protease gene. The primer thatroduces a 3' BglIs site into the gene. The amplified gene was used in the construction of homology vector 904-65.B7, which was used to insert foreign DNA into swinepox virus (SPV). The invention relates to a recombinant virus, e.g. SPV, that contains at least one foreign nucleic acid, inserted into a nonessential genomic region, that encodes feline CD28, CD80, CD86 or CTLA-4 protein, or their immunogenic fragments, and is expressed when the recombinant virus is introduced into a suitable encoding an immunogen derived from a feline pathogen such as FIV. It is used to enhance an immune response in a feline, particularly as a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cat, CD28, CD80, CTLA-4, CD86; immunogen; vaccine; viral infection; feline immunodeficiency disease; feline infectious peritonitis; feline intectious peritonitis; feline interest degenerative disease; autoimmune disease; virucide; immunomodulator; cytostatic; immunodeficiency; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                          Novel recombinant virus useful as immunomodulators, particularly in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eline influenza virus gag/protease gene PCR primer 11/94-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 12; DB 3; Length 28; 100.0%; Pred. No. 8.7e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 28 BP; 4 A; 9 C; 4 G; 11 T; 0 U; 0 Other;
                                                                                                                             (SCHE ) SCHERING-PLOUGH LTD.
(SCHE ) SCHERING-PLOUGH VETERINARY CORP.
                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 60; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL46912 standard; DNA; 28 BP.
                                             99WO-US009504
                                                                                          98US-00071711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(revised)
(first entry)
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAAAGTAAAA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 GGAAAGTAAAA 16
                                                                                                                                                                                                     Winslow BJ, Cochran MD,
                                                                                                                                                                                                                                               WPI; 2000-062155/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2002051792-A1.
                                               30-APR-1999;
                                                                                          01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAY-2002.
  11-NOV-11999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-AUG-2003
07-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAL46912;
                                                                                                                                                                                                                                                                                                                    vaccines
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ઠ d Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.

Leach M;

Shimkets RA,

99US-00303040.

30-APR-1999; 01-MAY-1998;

Viruses

98US-0083870P

Winslow BJ, Cochran MD;

(WINS/) WINSLOW B J. (COCH/) COCHRAN M D.

WPI; 2001-465210/50.

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Gaps

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Gaps

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0; Indels Length

Mismatches

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100.0%; Score 12; DB 4; I 100.0%; Pred. No. 8.6e+03;

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was used to determine precisely where on the VRE IRF-7 acts
                               Sequence 58 BP; 31 A; 6 C; 14 G; 7 T; 0 U; 0 Other;
                                                                                                Conservative
                                                                                                                              1 GGAAAGTAAAAA 12
                                                                                                                                                             12 GGAAAGTAAAA 23
                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                            09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP-2000
                                                                                              12;
                                                                                                                                                                                                                                                                               AAC98261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                             RESULT 10
AAC98261
                                                                                                Matches
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                                                                                                                                                             셤
                           The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apolymorsas, oncogenes, histories, kinases, colony stimulating factors, complement related proteins, cadherin, cyclin, polymerase, oncogenes, histories, kinases, colony stimulating factors, complement related proteins cytochromes, kinesins, cytokines, interferons, interleukins, Grand protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Discorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's diseases), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidhey, leukaemia), diseases of the nervous system and an infection of pathogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to controlling the level of Type 1 interferon expression by modulating the level of interferon regulatory factor (IRP)-7 or its functional analogue. This is useful for manufacturing a medicament for treating a condition in which an increase in interferon-alpha is beneficial, such as human viral infections or cancer. The method may also be used in the preparation of DNA vaccines for treating viral, bacterial and parasitic infections. The present sequence is the interferon alpha Al promoter VRE mutant 4PM. This mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Controlling Type I interferon expression level involves modulating level of interferon regulatory factor 7 or its functional analogue which is useful for treating human viral infections or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interferon alpha; IFN; Al promoter; virus responsive element; VRE; interferon regulatory factor; IRF-7; infection; cancer; DNA vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                         100.0%; Score 12; DB 4; Length 48; 100.0%; Pred. No. 8.6e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                              Sequence 48 BP; 7 A; 9 C; 1 G; 31 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interferon alpha Al promoter VRE mutant 4PM.
   Claim 1; Page 2369; 4143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Au WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Fig 2; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF77183 standard; DNA; 58 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-SEP-2000; 2000WO-GB003367.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Marches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeow WS,
                                                                                                                                                                                                                                                                                                                                                                                                              1 GGAAAGTAAAA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAAAGTAAAAA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-244558/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200118039-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2001
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                                                                                                                                                                                                                                                                                  organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF77183;
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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The called human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, wounds, renal disorders, reproductive disorders, immune system cardiovascular disorders, AAC99744 to AAC99772 and AAB54007 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer.
                                                                                                                                                                                                                                                                                                                                                                        Human, colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antilnfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder;
                                                                                                                                                                                                                                                                           Human colon cancer antigen nucleotide sequence SEQ ID NO:271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 141 BP; 42 A; 25 C; 28 G; 40 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infectious disease; cardiovascular disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 695; 2104pp; English.
AAC98261 standard; cDNA; 141 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAR-2000; 2000WO-US005883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0124270P
                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-587534/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAB53504
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100.0%; Score 12; DB 3; Length 141;

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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                              Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, single exon nucleic acid probe, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia; coronary heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 12; DB 4; Length 168; 100.0%; Pred. No. 8.6e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; SEQ ID NO 23318; 639pp + Sequence Listing; English
                                                                                                         Human foetal liver single exon nucleic acid probe #23318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 168 BP; 38 A; 45 C; 37 G; 48 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human liver single exon probe, SEQ ID No 24271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000; 2000US-0180312P.
26-MY-2000; 2000US-0207456F.
30-UTN-2000; 2000US-0069408.
03-AUG-2000; 2000US-0033366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US000669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABS49281 standard; DNA; 168
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                                                                       (first entry)
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ses 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483447/52
                                                                                                                                                                                                                                  WO200157277-A2.
                                                                                                                                                                                             Homo sapiens
                                                                       01-FEB-2002
                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABS49281;
                                ABA75013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample or determining the expression profile of a is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the protein sequences in ABB57020 to ABB57374) or by determining the protein expression profile of a gene group comprising these genes. The expression indicator when screening for ischaemic condition-improving drugs or therapeuting for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                           Mouse, ischaemia, compressive ischaemia; occlusive ischaemia; vasospastic ischaemia, ischaemic condition, ischaemic disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                       Mouse ischaemic condition related cDNA sequence SEQ ID NO:468
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                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takahashi Y, Nagata T, Ishii Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 151 BP; 40 A; 36 C; 36 G; 39 T; 0 U; 0 Other;
               Pred. No. 8.6e+03;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 1297; 2690pp; English.
100.08; Fig.
                                                                                                                                                                                                                  ABI99496 standard; cDNA; 151 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-2001; 2001WO-JP004192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-2000; 2000JP-00145977
                                                                                                                                                                                                                                                                                                07-MAR-2002 (first entry)
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                                    12; Conservative
                                                                                                               79 GGAAAGTAAAA 90
                                                                         1 GGAAAGTAAAAA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishikawa K, Asai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-034733/04.
                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200188188-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-NOV-2001
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                                                                                                                                                                                                                                                           ABI99496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes.
                                    Matches
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ABI99496
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Gaps

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WO200157273-A2 Homo sapiens.

ABA75013 standard; DNA; 168 BP.

RESULT 12 ABA75013/c ID ABA750

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thale cress; gene; ds; genetic manipulation; plant; biosynthesis; genetic modification; envixonmental stress; disease resistance; fungicide; insecticide; stress tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 12; DB 5; Length 177; 100.0%; Pred. No. 8.6e+03; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 177 BP; 41 A; 37 C; 42 G; 48 T; 0 U; 9 Other;
                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana polynucleotide #220.
                                                                                                                                                                                                                                                                                                                     Claim 1; Page 1191; 11750pp; English
                                                                                                                                                     Schlegel R, Endege WO, Monahan JE;
25-MAY-2000; 2000US-0207454P.
09-UUN-2000; 2000US-0211314P.
18-UUL-2000; 2000US-029007P.
13-DEC-2000; 2000US-0255281P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABX60874 standard; DNA; 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
1es 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 GGAAAGTAAAA 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMILTON C M.
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HARGISS T R.
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                                                                                                                                                                                         WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GORL/) GORLACH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2002142319-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABX60874;
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(HARG/)
(YUYY/)
(RAME/)
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements / fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in generic liver diseases such as cirrhosis, hyperlipotocteinaemia, hyperlipidaemia and hypercholestericles which is associated with coronary heart disease. ABS25011-ABS51005 represent human sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 12; DB 4; Length 168; 100.0%; Pred. No. 8.6e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 168 BP; 38 A; 45 C; 37 G; 48 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate expression marker cDNA 7359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; SEQ ID NO 24271; 658pp; English.
                                                                                                                                                                                                                                                                                                                              Penn SG, Hanzel DK, Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABV07368 standard; cDNA; 177 BP
                                                                                                           04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0207456F.
30-UTN-2000; 2000US-00609408.
03-AUG-2000; 2000US-0033366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-0032459P.
                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-FEB-2000; 2000US-0183319P.
16-MAR-2000; 2000US-0189862P.
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                                                                       30-JAN-2001; 2001WO-US000664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 GGAAAGTAAAA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAAAGTAAAAA 12
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-488898/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200160860-A2.
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                                09-AUG-2001
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RESULT 14

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The invention relates to Arabidopsis thaliana nucleic acid sequences. The DNA sequences and the polypeptides they encode are useful for identifying chandogous or related genes, for producing compositions that modulate the expression or function of the polypeptides, for mapping functional compositions of the protein, in diagnosis, for studying associated pathways, for genetic manipulation of cells, preferably plant cells, in screening assays of various plant strains to determine the strains that are capable of withstanding a particular disease or the strains that are capable of withstanding a particular disease or environmental strees, for enhancing or inhibiting production of compositions, such as plant cells and plants. Transgenic plants or transgenic organisms, such as plant cells and plants. Transgenic plants come in plants, screening biologically active agents, such as functional disease resistance and stress to cherance in plants, screening biologically active agents, such as functional diseases resistance and stress constructions of nutritional, commercial or medicinal value. Sequences ABX6065-ABX6154 represent Arabidopsis thaliana
                                                                                                                                                                                                                                                                                             Novel Arabidopsis thaliana nucleic acid useful for constructing a transgenic plant with enhanced disease resistance and enhanced traits of interest, as probes, and in diagnosis and screening purposes.
                                                                                                                                                 Gorlach J, An Y, Hamilton CM, Price JL, Hargiss TR, Yu Y;
Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
Garcia CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 12; DB 7; Length 181;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 181 BP; 60 A; 26 C; 25 G; 70 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 77; 277pp; English
                 MATHEW A V.
LEDFORD B L.
WOESSNER J P.
                                                                                                                                                                                                                                                       WPI; 2003-102509/09.
                                                                                       HAAS W D.
GARCIA C A.
                                                                 (WOES/)
(HAAS/)
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Search completed: March 25, 2004, 10:25:09 Job time : 16.4532 secs 31 GGAAAGTAAAA 42 g

1 GGAAAGTAAAA 12

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Sequence 30519, A Sequence 100, App Sequence 77849, A Sequence 8180, Ap Sequence 8180, Ap Sequence 373, App Sequence 373, App Sequence 373, App

30519, A 30519, A 100, App

Sequence 373, App Sequence 94822, A Sequence 750, App Sequence 77, Appl Sequence 371, Appl Sequence 14076, A Sequence 11968, Sequence 11968, Sequence 11968, Sequence 1246, App Sequence 1246, App Sequence 1246, App Sequence 105436, Sequence 1155, App Sequence 1155, App Sequence 1155, App Sequence 1159, App Sequence 1159, App Sequence 1159, App Sequence 119129,

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Mark D.
Recombinant Virus Expressing Foreign DNA Encoding
Feline CD80, Feline CD66, Feline CD28, Feline CTLA-4 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-098-263B-123886/c

Sequence 123886, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:
TILLE OF INVENTION: Human Microarray
FILE REFERENCE: 318.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT FILING DATE: 2001-08

FRIOR APPLICATION NUMBER: 60/276,759

FRIOR APPLICATION NUMBER: 60/276,759

FRIOR PILING DATE: 2001-03-16

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 25;
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2 US-10-085-783A-30519
5 US-10-085-783A-30519
1 US-10-082-825A-100
2 US-10-082-825A-100
2 US-10-424-599-77849
2 US-10-245-535A-8180
2 US-10-245-535A-8180
2 US-10-245-535A-8180
2 US-10-245-599-8668
2 US-10-424-599-95068
2 US-10-424-599-133130
2 US-10-424-599-133130
2 US-10-424-599-13559
2 US-10-424-599-13559
2 US-10-424-599-1559
2 US-10-424-599-1559
2 US-10-424-599-11669
2 US-10-424-599-11669
2 US-10-424-599-11669
2 US-10-424-599-11669
2 US-10-424-599-11668
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Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-917-800A-155
US-09-960-352-11484
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Patent No. USZ020151792A1
GENERAL INFORMATION:
APPLICANT: Winslow, Barbara J.
APPLICANT: Occhran, Mark
TITLE OF INVENTION: Recombinant Viru;
TITLE OF INVENTION: Reline CD80, Fel
       12
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CRGANISM: Homo sapien
US-10-098-263B-123886
     RESULT 2
US-09-303-040-80/c
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Sequence 271, App
Sequence 271, App
Sequence 472, App
Sequence 16691, A
Sequence 16691, A
Sequence 16691, A
Sequence 30575, A
Sequence 30575, A
Sequence 220, App
Sequence 22857, A
Sequence 2285, A
Sequence 2285, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 123886,
                                                                                                                       March 25, 2004, 10:03:04; Search time 10.395 Seconds (without alignments) 4297.861 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications Nh:*

1: /cgn2_6/prodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubpna/USO6_NEW_PUB.seq:*
3: /cgn2_6/prodata/1/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/prodata/1/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/prodata/1/pubpna/USO6_NEW_PUB.seq:*
6: /cgn2_6/prodata/1/pubpna/USO9_NEW_PUB.seq:*
7: /cgn2_6/prodata/1/pubpna/USO9_PUBCOMB.seq:*
8: /cgn2_6/prodata/1/pubpna/USO9_PUBCOMB.seq:*
10: /cgn2_6/prodata/1/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/prodata/1/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/prodata/1/pubpna/USO9_PUBCOMB.seq:*
13: /cgn2_6/prodata/1/pubpna/USO9_NEW_PUB.seq:*
13: /cgn2_6/prodata/1/pubpna/USO9_NEW_PUB.seq:*
14: /cgn2_6/prodata/1/pubpna/USO9_NEW_PUB.seq:*
15: /cgn2_6/prodata/1/pubpna/USO9_NEW_PUB.seq:*
16: /cgn2_6/prodata/1/pubpna/USO9_NEW_PUB.seq:*
16: /cgn2_6/prodata/1/pubpna/USO9_NEW_PUB.seq:*
17: /cgn2_6/prodata/1/pubpna/USO9_NEW_PUB.seq:*
16: /cgn2_6/prodata/1/pubpna/USO9_NEW_PUB.seq:*
16: /cgn2_6/prodata/1/pubpna/USO9_NEW_PUB.seq:*
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18: /cgn2_6/prodata/1/pubpna/USO9_NEW_PUB.seq:*
18: /cgn2_6/prodata/1/pubpna/USO9_NEW_PUB.seq:*
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-303-040-80
US-09-925-299-271
US-09-925-299-271
US-10-424-599-472
US-10-424-599-472
US-10-424-593-472
US-10-424-59-86937
US-10-424-59-86937
US-0-685-783A-16691
US-0-684-761-31340
US-0-684-761-31340
US-0-685-783A-30575
US-10-085-783A-30575
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US-10-424-599-52857
US-10-029-386-17951
US-10-424-599-75993
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                                                                                                                                                                                                                                                                                                                2458946 segs, 1861504846 residues
                                                                                                                                                                                        US-09-963-285-1_COPY_1692_1703
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                            nucleic search, using sw model
                                                                                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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RESULT 5
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Sequence 271, 4

Patent No. US20020055627A1

GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION:

FILE REFERENCE: PA.102

CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05883

PRIOR APPLICATION NUMBER: PCT/US00/05883

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1556

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 12; DB 9; Length 141; 100.0%; Pred. No. 1.2e+04; cive 0; Mismatches 0; Indels
TITLE OF INVENTION: Feline Interferon-gama And Uses Thereof FILE REFERENCE: 54957-B
CURRENT APPLICATION NUMBER: US/09/303,040
CURRENT FILING DATE: 1999-04-30
BARLIER APPLICATION NUMBER: 60/083,870
BARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 80
LENGTH: 28
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) LOCATION: (141)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (141)
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LOCATION: (13)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
LOCATION: (14)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
LOCATION: (25)
                                                                                                                                                                                                                               ; TYPE: DNA; CRGANISM: FIV PPR downstream primer US-09-303-040-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (12)
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US-09-925-299-271
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1 GGAAGTAAAA 12 ||||||||||| 79 GGAAGTAAAA 90

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 472
LENGTH: 149
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0
UB-09-92-299-271

Sequence 271, Application US/09925299

Publication No. US20030040617A9

GENERAL INPORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PAD-13-2001-08-10

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1556

SEQ ID NO 271

LENGTH: 141
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LOCATION: (1)..(149)
OTHER INFORMATION: unsure at all n locations
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-271
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
LOCATION: (39)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (13)
OTHER INFORMATION: n equals a,t,g, or NAME/ERY: misc_feature
LOCATION: (14)
OTHER INFORMATION: n equals a,t,g, or NAME/ERY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Sequence 472, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
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COGATION: (12)
CTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
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Best Local Similarity 100.
Matches 12, Conservative
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                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature LOCATION: (141)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Glycine max
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Publication No. US20040037841A1

GENERAL INFORMATION:

APPLICANT: Litew, C.C.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REPRENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085,783A

CURRENT APPLICATION NUMBER: US 60/236,340

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR APPLICATION NUMBER: US 60/271,955

NUMBER OF SEQ ID NOS: 58994
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Sequence 16691, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: ChondroGene Inc.
APPLICANT: ChondroGene Inc.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US 60/305,783
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
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                                                                                                    Length 149;
                                                                                                                                                     Indels
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_100426C.1
US-10-424-599-472
                                                                                                 100.0%; Score 12; DB 12;
100.0%; Pred. No. 1.2e+04;
tive 0; Mismatches 0;
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SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                       138 GGAAAGTAAAA 127
                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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US-10-085-783A-16691
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; ORGANISM: Human
US-10-085-783A-16691
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; ORGANISM: Human
US-10-242-535A-16691
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Sequence 11340, Application US/09864761

j Sequence 21340, Application US/09864761

j Patent No. US20020048763A1

general INFORMATION:
   APPLICANT: Rank, David R.
   APPLICANT: Hanzel, David R.
   APPLICANT: Hanzel, David R.
   APPLICANT: Hanzel, David R.
   APPLICANT: Hanzel, David R.
   APPLICANT: Chem. Wensheng
   TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
   FILE REFERENCE: Abenica-X-1
   CURRENT APPLICATION NUMBER: US 60/180,312
   PRIOR FILING DATE: 2000-05-26
   PRIOR PLING DATE: 2000-06-26
   PRIOR PLING DATE: 2000-06-36
   PRIOR PLING DATE: 2000-06-3
   PRIOR PLING DATE: 2000-09-37
   PRIOR PLING DATE: 2000-09-27
   PRIOR PLING DATE: 2000-09-27
   PRIOR PLING DATE: 2000-09-27
   PRIOR PLING DATE: 2000-09-27
   PRIOR PLING DATE: 2001-01-30
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                                                            Gaps
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; Sequence 86937, Application No. US20040031072A1
; GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwai
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION WUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
; WUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 86337
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      Length 150;
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100.0%; Pred. No. 1.2e+04;
cive 0; Mismatches 0;
   100.0%; Score 12; DB 15; 100.0%; Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_49514C.1
US-10-424-599-86937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(160)
OCHER INFORMATION: unsure at all n locations
FEATURE:
                                                            0; Mismatches
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Best Local Similarity 100.
Matches 12; Conservative
Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                   130 GCAAAGTAAAA 141
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APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REPRENCE: 4231,72005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT APPLICATION NUMBER: US 10/085,783
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-14
PRIOR FILING DATE: 2001-03-12
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illarity 100.0%; Pred. No. 1.2e+04;
Conservative 0; Mismatches 0; Indels
                                                                           Indels
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Parent No. US20020142319A1
GENERAL INFORMATION:
ITILE OF INVENTION: Expressed Sequences of Arabidopsis
CURRENT APPLICATION NUMBER: US/09/924,035A
CURRENT APPLICATION NUMBER: US 60/148,784
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 900
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 220
                                   Pred. No. 1.2e+04;
Mismatches 0;
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Pred. No. 1.2e+04;
; Mismatches 0;
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100.001 . ...
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Best Local Similarity 100.
....hes 12; Conservative
                                   Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ChondroGene Inc.
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Best Local Similarity
Matches 12; Conserv
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US-10-242-535A-30575
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US-10-085-783A-30575
; Sequence 30575, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: Chondroene Inc.
; APPLICANT: Chondroene Inc.
; APPLICANT: Liew, C.C.
; TILLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REPRENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR PRILING DATE: 2001-07-13
; PRIOR PLILING DATE: 2001-03-12
; PRIOR PLILING DATE: 2001-03-12
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PARENTIN Version 3.2
; SEQ ID NO 30575
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4
OTHER INFORMATION: NT HIT: D49387.1, EVALUE 5.006-90
OTHER INFORMATION: SWISSPROT HIT: Q14914, EVALUE 1.006-26
US-09-864-761-31340
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100.0%; Score 12; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
                 PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/774,203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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US-10-085-783A-30575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM:
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
Cao Vinua
APPLICANT:
Cao Vinua
APPLICANT:
TILE OF INVENTION:
Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 12; DB 12; 100.0%; Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_39636C.1
US-10-424-599-75993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Glycine max FEATURE:
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Fublication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, David R.
APPLICANT: Penn, David R.
APPLICANT: PENSTION: BXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFREADER: ASOUTH APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ 1D NO 17951
LENGTH: 206
                                                                  Sequence 52857, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
APPLICANT: La Roca Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Syn Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 285684
SEQ ID NO 52857
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 14
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 14
OTHER INFORMATION: NT HIT: gil5718689, EVALUE 2.00e-78
OTHER INFORMATION: SWISSEROT HIT: BP908569.1, EVALUE 1.00e-80
US-10-029-386-17951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 196;
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100.0%; Score 12; DB 14; Length 206;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 12; Conservative 0; Mismatches 0; Indels
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100.0%; Score 12; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Clone ID: PAT_MRT3847_18742C.1
US-10-424-599-52857
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US-10-424-599-75993
; Sequence 75993, Application US/10424599
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ORGANISM: Homo sapiens
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                                                       US-10-424-599-52857/c
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Gaps

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Title: Perfect score:

Sequence:

4

OM nucleic

Run on:

Scoring table:

Searched:

Minimum I Maximum I

Database

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Guss.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 37)

Islam, L., Aoyagi, A., Barber, M., Baccorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Londact: Robert B. Weiss

University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

94112, USA

Tel: 801 585 5177
CCG400241 01SC0561-0
CCD919593 GG08.1130
CCC049447 01SC058-0
EX547641 Arabidops
CCG846994 01SC0554-0
CCG64794 01SC0554-0
CCG663748 PULZ1U23.
ALS09743 vx23C04.7
AL942319 Arabidops
EHO78181 ARABIGOS
EHO78181 EROT-23-3
AL75935 Arabidops
EHO78181 ARABIGOS
EHO78181 EHO78195
EHO78181 ARABIGOS
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2M0212K19F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0212K19 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB290481
BI188234
BI191170
AV309354
                                                              BX547641
CG846984
AV8246914
CG063748
CF0846155
CF08403743
AIS09743
AIS09743
BH092319
BH495080
CG466358
BH685302
BH685302
BH865302
BH865302
BH865302
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CC048069
AZ043161
AU256208
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AL759355
BI452728
AZ889185
CG570474
AV354395
BM750390
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BZ487651
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GSS.
          0110000000160016001166110006101000611116616000
048000 004 080008000 0088 00088 0000 0 088
        AZ949109
          RESULT 1
AZ949109
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ949109 ZM0212K19
BQ078148 fy85b01.y
CG427224 0180726-0
BH850672 SALK_0716
                                                                                                                                           March 25, 2004, 09:53:09; Search time 90.6845 Seconds (without alignments) 3951.570 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                    55026578
                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                              27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                         US-09-963-285-1_COPY_1692_1703
12
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Maximum Match 100%
Listing first 45 summaries
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BQ078148
CG427224
BH850672
                                                                                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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3: em_esthum:*
5: em_esten:*
6: em_estpl:*
7: em_estro:*
8: em_estpl:*
10: 9b_est1:*
11: 9b_hc:*
11: 9b_est2:*
11: 9b_est2:*
11: 9b_est3:*
12: 9b_est3:*
13: 9b_est3:*
14: 9b_est2:*
15: em_estpl::*
16: em_estpl::*
16: em_gss_hum:*
16: em_gss_hum:*
17: em_gss_hum:*
18: em_gss_hum:*
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em gss rod: *
em gss phg: *
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gb_gssī:*
gb_gss2:*
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DB seq length: 200000000
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28
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Match Length DB
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65
67
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5

Score

No. Result

2222

H 01 10 4

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Email: zbrafish@watson.wustl.edu
cDNA Library construction by: Joe Barnes and Steve Johnson. DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution: RessourcenZentrumPrimarDatenbank, Berlin, Germany
(web address: www.rzpd.de)
Seq primer: T3 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG427224 66 bp DNA linear GSS 15-SEP-2003 01S0726-07A1-H10 UniformMu MuTAIL Library Zea mays genomic clone 01S0726-07A1-H10, genomic survey sequence.
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1 (bases 1 to 66)
Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
                                                                                                                                                                                                                                                                                                                                                                                                                                          /tienue_inverser.org.
/tienue_type="embryo, 14 somite"
/lab host="embryo, 14 somite embryo"
/clone lib="Zebrah Gis 14 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 65;
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100.0%; Pred. No. 3.3e+05;
/ative 0; Mismatches 0; Indels
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Plant Molecular and Cellular Biology Program
University of Florial
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322

    .65
/organism="Danio rerio"
/mol_type="mRNA"
/strain="C32"

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/clone="IMAGE:5816785"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG427224.1 GI:34735704
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Unpublished (2003)
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Best Local Similarity 100.
Matches 12; Conservative
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Zea mays
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CG427224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Bab.*Female."
/ Jab host="E" coli strain XL10-Gold, T1-resistant, F-"
/ clone_lib="Mouse 10kb plasmid UUGC2M library"
/ note="Vector: PWD42nr; Purified genomic DNA from M
musculus CG7BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
/ http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt enderrepaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides ware
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the linsert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (Jases 1 to 65)

2 Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood, K., Steptoc,M., Theising,B., Allan,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., WashU Zebrafish EST Project 1998

L Onpublished (1998)

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 bp mRNA linear EST 02-APR-2002
fy85b01.y1 Zebrafish C32 14 somite embryo Danio rerio cDNA clone
BQ078148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: K column: 19
Seg primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 37.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0212K19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        'sex="Female"
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G608.113005F010910 G608 Triticum aestivum cDNA clone G608113005, mbNA sequence. CD119593. G1:32767357 EST 15-JUL-2003 EST.
                                                                                                                                                                                                                                                                    CG400241 13 bp DNA linear GSS 02-SEP-2003 01S0561-04A1-H12 UniformMu MuTAIL Library Zea mays genomic clone 01S0561-04A1-H12, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="Uniformum WITAIL Library"
//clone lib="Uniformum WITAIL Library"
//note="Vector: TOPO-PCR4; DNA fianking Mu transposon
//note="Vector: TOPO-PCR4; DNA fianking
//note="Vector topolation of the thermo assymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted respeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."
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1 (bases 1 to 73)
Latshaw,S., Tan,B..C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        population
Unpublished (2003)
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
Po 11690 Gainesville, Ft 32611-0690, USA
Tel: 352-392-1228 x322
Email: drm@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line: 0150561-04, Primer set: A
Class: transposon insertion site.
Location/Qualifiers
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  Length 67;
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100.0%; Pred. No. 3.2e+05;
ive 0; Mismatches 0;
100.0%; Score 12; DB 28;
100.0%; Pred. No. 3.3e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_trype="genomic DNA"
/mol_trein="W22 (ACR, Dz1-m9)"
/cultivar="UniformW1"
/db xref="taxon:4577"
/clone="0180561-04A1-H12"
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Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .73
/organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                              CG400241.1 GI:34399125 GSS.
     Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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12; Conserv?
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Zea mays
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CG400241
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CD919593
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; core eudicots;
rosids; eurosids II; Brassicales; Brassicacea; Arabidopsis.

1 (bases I to 67)
2E I (bases I to 67)
3E Alonso,J.M., Leske,A., Karnes,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Frednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH850672 67 bp DNA linear GSS 13-JUN-2002 SALK 071670.53.75.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_071670.53.75.x, genomic
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/clone="SALK 0716.70.53.75.x"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                         /db_xref="taxon:4577"

/db_xref="taxon:4577"

/clone="10180726-0714.H10"

/clone="Vector: TOPO-PCR4; DNA flanking Mu transposon

/insertions in Mu inactive lines were extracted from the

UniformMu maize population by the thermo assymmetric

interlaced PCR (TAIL) protocol using primers specific for

the Mu terminal inverted repeat and a set of 16 arbitrary

primers. Amplicons were size enriched using Sepharose 400

spin columns and cloned into the TOPO PCR4 vector."
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100.0%; Pred. No. 3.3e+05;
ive 0; Mismatches 0;
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/mol_type="genomic DNA"
/strain="Columbia 0"
                                                    /mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: TDNA tagged.
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Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; Pooideae; Irticeae; Triticum.
(boaideae; Triticeae; Triticum.
(cases 1 to 78)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoldeae, Andropogoneae, Zea.

1 (bases 1 to 81)
Latshaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
                                                                                      Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                     This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Floride, FL 32611-0690, USA
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmoufl.edu
Sequence flanking probable Mu insertion site in UniformMu line: 01S-458-3
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/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
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/mol_type="mRNA"
/db_xref="taxon:4565"
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/olone="gre="grain (608 degrees per day after pollination)"
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                                                                                                                                                                         93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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Unpublished (2003)
Conteat: Donald R. McCarty
Plant Molecular and Cellular Biology Program
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100.0%; Pred. No. 3.1e+05;
ive 0; Mismatches 0;
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/strain="W22 (ACR, bz1-m9)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_lib="G608"
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Best Local Similarity 100.
Matches 12, Conservative
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                                                                              Genoplante.
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CC049447
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
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/clone="GK-546F08-020630"
/clone="ib="Axabidopsis thaliana T-DNA insertion lines"
/clone="ip="tcaxon:3702"
/clone="ip="tcaxon
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Direct Submission

Direct Submission

Submitted (Od. 701-2003) Weisshaar B., Max-Planck-Institut fuer
Submitted (Od. 701-2003) Weisshaar B., Max-Planck-Institut fuer
Subchtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene Ar3902040. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:

Location/Qualifiers
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insertions in Mu inactive lines were extracted from the UniformMu maize population by the thermo assymmetric interlaced PCR (TAIL) protocol using primers specific for the Mu terminal inverted repeat and a set of 16 arbitrary primers. Amplicons were size enriched using Sepharose 400 spin columns and cloned into the TOPO PCR4 vector."
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Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Unpublished
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100.0%; Pred. No. 3e+05;
ive 0; Mismatches 0;
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BX547641.1 GI:32440450
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Best Local &
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BX547641/c
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KEYWORDS
SOURCE
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae,
Pooideae, Triticeae, Hordeum.
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1 (bases 1 to 105)

Mittelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="leaves"
/dev stage="vegetative stage"
/clone lib="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare leaves vegetative stage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CG063748 10.6_1.0_KB Zea mays genomic clone ZMMBTa0537F14,
                                                                                                                     Barley. EST sequencing project in NIG and Okayama Univ Unpublished (2001)
Contact: Kazuhiro Sato
Research Institute for Bioresources
Chayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazasto@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/barley/
Sato, K., Salsho, D., Takeda, K., Shini, T. and Kohara, Y. Direct submission;
                                                                                                                                                                                                                                                                                                                                                         database.http://www.shigen.nig.ac.jp/barley/Barley.html.
Location/Qualifiers
1..102
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                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Akashinriki"
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; Pred. No. 2.7e+05;
0; Mismatches 0;
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/mol_type="genomic DNA"
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    Hordeum vulgare subsp. vulgare
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Class: sheared ends.
Location/Qualifiers
1..105
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Unpublished (2003)
Other GSSs: PUIAH31TD
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence. CG063748
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Best Local Similarity 100.
Matches 12; Conservative
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AUTHORS
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CG063748
LOCUS
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insertions in Mu inactive lines were extracted from the
UniformNu maize population by the thermo assymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers, Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."
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AV832401. GI:14524490
                                                                                                                                                                                                                                                CG846984 11-NOV-2003 17-NOV-2003 01S0554-03C1-CO7 UniformMu MuTAIL Library Zea mays genomic clone 01S0554-03C1-CO7, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Donald R. McCarty
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
Po 110690 Gainesville, FL 32611-0690, USA
Tel: 325-332-1928 x322
Email: drimeul.edu
Sequence flanking probable Mu insertion site in UniformMu line:
0180554-03, Primer set: C
Class: transposon insertion site.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 94)
Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
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Query Match 100.0%; Score 12; DB 29; Length 85; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 12; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.8e+05;
ive 0; Mismatches 0;
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Hordeum vulgare subsp. vulgare
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GSS 19-AUG-2003

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Gaps

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Helianthus paradoxus
Helianthus paradoxus
Helianthus paradoxus
Helianthus paradoxus
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Heliantheae; Helianthus.

E (bases I to 11)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Eliison,P., Kolkman,J., Lavelle,D., Chevalier,P., Ziegle,J.,
Eliison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Iai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.com/
QHL21J23.yg.abl QH L sunflower H.paradoxus (salt stress) Helianthus paradoxus cDNA clone QHL21J23, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 12-MAR-1999
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/clone_lib="QH_L sunflower H.paradoxus (salt stress)"

/clone_lib="QH_L sunflower H.parary was constructed from

four different sources (seedling, root, leaf and flower)

of RNA from a single genotype. cDNAs were pooled and

cloned into a high-copy vector pGBN-T. Details of library

construction can be obtained at http://cgpdb.ucdavis.edu/
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Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 112)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Alexander Kozik (R.W.Michelmore)
Department of Vegetable Crops, R.W.Michelmore Lab
Department of Vegetable Crops, R.W.Michelmore Lab
Minversity of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Pax: 1-(530)-752-9659
Fax: 1-(530)-752-9
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Unpublished (1997)
Contact: Nobert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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vx23d04.yl Soares thymus 2NbMT Mus musculus cDNA clone
IMAGE:1265287 5', mRNA sequence.
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/mol_type="mRXRA"
/do_xref="taxon:73304"
/clone="QHL21023"
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Location/Qualifiers
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AI509743.1 GI:4408648
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AI509743
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/mol_type="genomic DNA"
/estrain="W32 (ACF, bz1-mg)"
/cultivar="UniformVu"
/db xref="taxon:4577"
/clone="105579-09A1-H10"
/clone="105579-09A1-H10"
/clone="105579-09A1-H10"
/clone="IberUniformVu MuTAIL Library"
/clone="ToPO-PCR4; DNA flanking Mu transposon
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
/note="Vector: ToPO-
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
        /db_xref="taxon:4577"
/clone="ZMMBTa0537F14"
/clone="Ib="ZM_0.6_1.0_KB"
/clone lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4_TOP0, Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA_library"
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0180579-09A1-H10 UniformWu MuTAIL Library Zea mays genomic clone 0180579-09A1-H10, genomic survey sequence.
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Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 332-3292-1928 x322
Email: drawaffl.edu
Sequence flanking probable Mu insertion site in UniformMu line: 0150579-09, Primer set: A
Class: transposon insertion site.
Location/Qualifiers
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Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
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Search completed: March 25, 2004, 15:29:59 Job time: 95.6845 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Thymus"
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/clone_lib="DH10B"
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/note:"Vector: pt7T3D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3/]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
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                                                     This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the correct orientation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosso, M., Strizhov, M., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B., A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ווהפסל inear GSS 24-OCT אתם 113 bp DNA linear GSS 24-OCT Arabidopsis thaliana T-DNA flanking sequence GK-265All-01499B, מאוקטלומהול sequence GK-265All-01499B, Allo42310
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(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
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Li,Y., Strizhov,N., Rosso,M. and Weisshaar,B.
Direct Submission
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100.0%; Pred. No. 2.6e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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Arabidopsis thaliana
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Location/Qualifiers
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Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/. Location/Qualifiers
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AA330856 v271C06.8
AU255210 AU255210
BZ52714 2M0103102
AZ401018 1M0167K04
AZ401018 1M0167K04
AZ46306 Arabidops
AL946600 Arabidops
AZ6131104 £677064.9
AZ618897 2M0089N10
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BH911549 SALK 0693
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AZ806355 2M0011K20
AZ806355 2M0011K2035
AR60618 VMM6802986
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BK51171 Arabidops
AL751753 Arabidops
BH864357 SALK 0958
CC888324 SALK 1516
AL764318 Arabidops
AU255936 AU255936
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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AI931104
AZ617367
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BH906176
AU257598
BH864657
AU254247
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CC795092
AU102686
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BH911549
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AZ417527
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Mus musculus
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AZ465994.1 GI:10624119
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Unpublished (2000)
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Tel: 801 585 5606
Fax: 801 585 7177
   RESULT 1
AZ465994/c
LOCUS
DEFINITION
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ORGANISM
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AZ481958 1M0306G07
AZ663647 1M0543G20
AL479789 T. brucei
                                                                                               March 25, 2004, 09:53:09; Search time 68.0134 Seconds (without alignments) 3951.570 Million cell updates/sec
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                    nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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/GEAS="MODE" Coli strain XLIO-Gold, Tl-resistant, F-"
/Glob hose="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/Glob ilb="Mouse libkb plasmid UUGCIM library"
/note="Wedcor: PWD42hry; Purified genomic DNA from M.
/note="Wedcor: PWD42hry; Purified genomic DNA from M.
/note="Wedcor: PWD42hry; Purified genomic DNA from M.
Laboratory Mouse DNA Resource from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarces gal
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMOBASCO MOUSE 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0543G20 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 24)
Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Niederhausern, A. and Wright, D., Weise, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weise, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 9; DB 28; Length 24; Best Local Similarity 100.0%; Pred. No. 1.7e+05; Matches 9; Conservative 0; Mismatches 0; Indels
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0306 row: G column: 07
Seg primer: CACACAGGAAACAGCTATGACC
Class: plaemid ends
High quality sequence stop: 24.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:10090"
/clone="UUGC1M0306G07"
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Fax: 801 585 7177
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84112, USA
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AZ663647
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Mus musculus (house mouse)

Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.

Essas 1 to 24)

Sunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmud,M., Menen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederinausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

University of Utah Genome Center

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                /Bab. Maid.
/ Jab. hoste-E. Coli strain XL10-Gold, T1-resistant, F-"
/ clone_lib="Mouse 10kb plasmid UUGCIM library"
/ clone_lib="Mouse 10kb plasmid UUGCIM library"
/ note=="Weator: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (Accuments/Anares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated by resease and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0276 row: O column: 15
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                      sex="Male"
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Best Local Similarity
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AZ481958/c
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COMMENT
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The Character of the Control of the Control of the Control of the Control of 
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/clone="SALK 095812"
/clone="SALK 095812"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Beal: nelsayed@cigr.org
Email: nelsayed@cigr.org
at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Location/Qualifiers
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100.0%; Pred. No. 1.7e+05;
tive 0; Mismatches 0;
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Pred. No. 1.7e+05;
O; Mismatches 0;
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/db_xref="texon:5691"
/clone="212f07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (thale cress)
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100.0%; Pred. No.
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/mol_type="genomic DNA"
/strain="Columbia 0"
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BH864357.1 GI:22100255
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Best Local S
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BH864357/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil 4732114 (gb| AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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I (bases 1 to 25)

E 1 (bases 1 to 25)

Hall, N. Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Rockville, MD. Genomic DNA isolated from a cloned population of
to give a tight size distribution (
to give a tight size distribution (
to k). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
/lab host="B. Coli strain Xiilo-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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T. brucei sheared genomic DNA clone 212f07, forward sequence,
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Eukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae,
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Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0543 row: G column: 20
Seq primer: GGTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
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    .24
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                     /db xref="taxon:10090"
/clone="UUGC1M0543G20"
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GSS.
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/strain="Columbia 0."
/db.xref="taxon:3702"
/dlone="GK-124006-012813"
/clone="Inb="Arabidopsis thaliana T-DNA insertion lines"
/clone="Inb="Arabidopsis thaliana T-DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAG161. The lines contain one or more T-DNA from vector pAG161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                                                                                                                                            Sosso, M., Strizhov, N., Li, Y. and Weisshaar, B.

Direct Submission
Submitted (17-JUW-2002) Weisshaar B., Max-Planck-Institut fuer
Submitted (17-JUW-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl won-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene At1970560. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
Location/Qualifiers
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AU255936 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0006850 3', mRNA sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                            Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                                                                               Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                          A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
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Kato,K. and Marcba,R.
Generation of expressed sequence tags from mouse brain Unpublished (2002)
Contact: Kikuya Kato
Graduact: Kikuya Kato
Graduact School of Biological Sciences
Nara Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 9; DB 29; Length 31; Best Local Similarity 100.0%; Pred. No. 1.7e+05; Matches 9; Conservative 0; Mismatches 0; Indels
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AU255936.1 GI:20319148
                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 31)
                                                                                                              and Weisshaar, B.
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Arabidopsis thaliana T-DNA flanking sequence GK-124C06-012813,
genomic survey sequence..
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                                                                                                                                                                                                                  CC888324 151694.27.60.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana Genomic clone SALK 151694.27.60.x, genomic Arabidopsis thaliana genomic clone SALK 151694.27.60.x, genomic
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/clone="SALK 151694.27.60.x"
/clone="Ib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
Bukaryota, Viridplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 26)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Adonso,J.W., Leisse,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is single pass sequence recovered from the left border of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 558 6379
Email: ecker@salk.edu
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100.0%; Pred. No. 1.7e+05;
cive 0; Mismatches 0;
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/strain="Columbia 0"
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Class: TDNA tagged.
Location/Qualifiers
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CC888324
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| ACAATGTT 10
                                                                                     ACAAATGTT 11
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Matches 9; Conserv
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BZ597035 19.00.n Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_099290.19.00.n, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 34)
Kato, K. and Matoba, R. Generation of expressed sequence tags from mouse brain Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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/clone_lib="3'-directed mouse cDNA library"
                                                                                                                                                                                                                                                                                                                            100.0%; Score 9; DB 9; Length 34; 100.0%; Pred. No. 1.7e+05;
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Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5589
Email: Kato©bsaist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp,
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0004806"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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AU255210.1 GI:20317731
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Matches 9, Conservative
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Best Local Similarity
Matches 9; Conserv
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AU255210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA930856 31 Soares mammary gland NbWAG Mus musculus cDNA clone IMAGE:1331914 3' similar to SW:UBSC HUMAN P47986 AA930856 AA930856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The washU-HMI Mouse EST Project
The washU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashI-HMI Mouse EST Project
WashI-HMI Mouse EST Project
WashI-HMI Wash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
Mus musculus
Mus musculus
Mus musculus
Mus musculus
Mus musculus
Muscaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musria
1 (Dases I to 34)
Marra, M.; Hillier, L., Allen, M.; Bowles, M.; Dietrich, N.; Dubuque, T.;
Geisel, S.; Kucaba, T.; Lacy, M.; Le, M.; Martin, J.; Morris, M.;
Schellenberg, K.; Steptoe, M.; Tan, F.; Underwood, K.; Moore, B.;
Theising, B.; Wylie, T.; Lennon, G.; Soares, B.; Wilson, R. and
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/note="Organ: mammary gland; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/db_xxef="teaxon:10090"
/clone="BED06850"
/clssue type="brain"
/clone_lib="3'-directed mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 9; DB 9; Length 33; 100.0%; Pred. No. 1.7e+05; Live 0; Mismatches 0; Indels.
8916-5 Takayama, Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: ktato@bs.ist-nara.ac.jp,
URL:http://lovez.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers
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/dev_stage="4 weeks"
/lab_host="DH10B"
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/clone="IMAGE:1331914"
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/strain="C57BL/6J"
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nes 9; Conservative
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Gaps

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Mus musculus (mode)

Endaracia, Chordata; Craniata; Vertebrata; Euteleostomi;

Endaracia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (Dases 1 to 40)

E Junn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacree,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weise,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah Blomers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gelectrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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40 bp DNA linear GSS 03-OCT-2000
1M0167K04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0167K04 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                            /db xref="taxon:10090" /db xref="taxon:10090" /clone="UUGC2M0103H02" /dsex="Male" /lab host="E. Coli strain XL10-Gold, Tl-resistant, F-" /lab host="E. Coli strain XL10-Gold, Tl-resistant, F-" /note="Vector: PWP42nv; Purified genomic DNA from M. musculus G75E/64 (male) was obtained from the Jackson /laboratory Mouse DNA Resource,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 9; DB 28; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: H column: 02
Seg primer: CACACAGGAAACAGCTATGACC
Class: pleamid ends
High quality sequence stop: 37.
Location/Qualifiers
                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/67"
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AZ401018.1 GI:10516092
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Fax: 801 585 7177
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                              Eukaryota; Viridiantes; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 34)
Salomso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shim,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 658 479 4100 x1752
Fax: 858 658 6379
Email: ecker@alk.
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2M0103H02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0103H02 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db xref="taxon:3702"
/clone="SALK 099290.19.00.n"
/clone="SALK 099290.19.00.n"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Was musculus

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases I to 37)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Relly,M., Rose,M., Rose,M., Rose,R.,

Modesthausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 306), Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia 0"
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AZ827214.1 GI:12997122
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: TDNA tagged
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Fax: 801 585 7177
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Gaps . 0

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligomuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL946600 42 bp DNA linear GSS 24-OCT-2002
Arabidopsis thaliana T-DNA flanking sequence GK-297G01-015513,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished (GABI-Kat) (Asses 1 to 42)

Rosso,M., Li,Y., Strizhov,N. and Weisshaar,B.
                                                                                                                                                                                                                                                                                                                                                  /lab.host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note=""Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H. and Weisshaar,B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 9; DB 28; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Exror: 0.00
Plate: 0273 row: J column: 07
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 41.
                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/60"
                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC1M0273J07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic survey sequence. AL946600
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Miderhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plannid in merte.
                                                                                                                                                                                                                                                                                                                       /sex="Male"
/sex="Male"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIN library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
Laboratory Mouse DNA Resource
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                     Insert Length: 10000 Std Brror: 0.00 Plate: 0167 row: K column: 04 Seg primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 40. Location/Qualifiers
                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="c57BL/60"
/db xref="taxon:10090"
/clone="UUGCIM0167K04"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
  Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ACAAATGTT 12
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Direct Submission

JOURNAL Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer

JOURNAL Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer

Lucchtungsforschung, Carl-von-Linn-Weg 10, Koch, 50829, German

This sequence is recovered from the left border of the T-DNA. It

indicates an insertion close to or within gene A-4915370. The

sequences are generated at the WD1 for Plant Breeding Research in

the context of the GABI-KAt project. GABI-KAt is part of the German

the context of the GABI-KAT project. GABI-KAT is part of the German

blant Genomics program designated 'GABI'. Information on line

the context of the GABI-KAT project. GABI-KAT /

Location/Qualifiers

source

//coanism="Arabidopsis thaliana"
//strain="Columbia O"
//db.xref="teamonic" DNA"
//strain-"columbia O"
//db.xref="teamonic" DNA"
//done lib="Arabidopsis thaliana T-DNA from T-DNA
//done lib="Arabidopsis thaliana T-DNA from The DNA
//done lib="teamonic" DNA
//done lib="tea
```

Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

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Db 13 ACAAATGTT 21 Search completed: March 25, 2004, 15:30:04 Job time: 73.0134 secs

1 ACAAATGTT 9

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Sequence 23316, 7
Sequence 23517, 8
Sequence 24518, A
Sequence 44365, A
Sequence 47225, A
Sequence 47225, A
Sequence 74037, A
Sequence 74037, A
Sequence 81113, A
Sequence 81120, A
Sequence 81120, A
Sequence 8120, A
Sequence 8121, A
Sequence 89911, A
Sequence 89911, A
Sequence 105011, A
Sequence 105011, A
Sequence 105011, Sequence 105012, Sequence 105012, Sequence 105012, Sequence 105012, Sequence 125835, Sequence 1012, Appl

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Query Match
100.0%; Score 9; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.6e+04;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-370-860A,
Sequence 14, Application US/10370860A,
Publication No. US20030219791A1
GENERAL INFORMATION:
APPLICANT: NOVO NORDISK A/S
APPLICANT: Wahl, Philip
APPLICANT: Wahl, Philip
APPLICANT: Grondahl, Christian
APPLICANT: Seennicke, Vibeke Westphal
FILIK OF INVERTION NUMBER: US/10/370,860A
PRIOR APPLICATION NUMBER: 09/231,670
PRIOR APPLICATION NUMBER: O9/334,948
PRIOR APPLICATION NUMBER: PA 2002 00277
PRIOR APPLICATION NUMBER: PCT/DK01/00550
PRIOR APPLICATION NUMBER: PA 2000 01259
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-08-25
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 14
SEQ ID NO 14
US-10-098-263B-23315

US-10-098-263B-23316

US-10-098-263B-23517

US-10-098-263B-40465

US-10-098-263B-47365

US-10-098-263B-47365

US-10-098-263B-47716

US-10-098-263B-47716

US-10-098-263B-37711

US-10-098-263B-37711

US-10-098-263B-37711

US-10-098-263B-311120

US-10-098-263B-311120

US-10-098-263B-31120

US-10-098-263B-31251

US-10-098-263B-3977

US-10-098-263B-3977

US-10-098-263B-3977

US-10-098-263B-105011

US-10-098-263B-105011

US-10-098-263B-105011

US-10-098-263B-105011

US-10-098-263B-105011

US-10-098-263B-105011

US-10-098-263B-105011

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US-10-098-263B-105011

US-10-098-263B-105011
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ORGANISM: Artificial Sequence
    OTHER INFORMATION: Synthetic US-10-370-860A-14
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Sequence 84, Appl
Sequence 57, Appl
Sequence 286, Appl
Sequence 4249, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 1149, Appl
Sequence 15021, Appl
Sequence 15021, Appl
Sequence 15021, Appl
Sequence 15021, Appl
                                                                                            March 25, 2004, 10:03:04; Search time 7.79622 Seconds (without alignments) 4297.861 Million cell updates/sec
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Sequence
Sequence
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1: \cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: \cgn2_6/ptodata/1/pubpna/PCI \mathbb{NEM_PUB.seq:*}

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18: \cgn2_6/ptodata/1/pubpna/US60 \mathbb{NEM_PUB.seq:*}

18: \cgn2_6/ptodata/1/pubpna/US60 \mathbb{NEM_PUB.seq:*}
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                              2458946 segs, 1861504846 residues
                                                                                                                                                        US-09-963-285-1_COPY_223_231
9
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Maximum Match 100%
Listing first 45 summaries
                                                                        - nucleic search, using sw model
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Maximum DB seq length: 200000000
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ALIGNMENTS

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APPLICANT: Picard, Francis J.
APPLICANT: Paracis J.
APPLICANT: Picard, Francis J.
APPLICANT: Poullette, Marc
APPLICANT: Outlette, Marc
APPLICANT: Noy, Paul H.
TITLE OF INVENTION: Species Specific, Genus-Specific and Universal DNA
TITLE OF INVENTION: Probes and Amplification Primers to Rapidly Detect
TITLE OF INVENTION: Associated Antibictic Resistance Genes from
TITLE OF INVENTION: Associated Antibictic Resistance Genes from
FILE REPERENCE: 12287.29
CURRENT APPLICATION NUMBER: US/09/889,643
CURRENT BLING DATE: 2001-11-20
PRIOR PILING DATE: EARLIER FILING DATE: 1999-05-09
PRIOR FILING DATE: EARLIER FILING DATE: 1996-11-04
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 84
LENGTH: 22
LENGTH: 22
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APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Casman, Stacie J.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gangolli, Beha A.
APPLICANT: Stone, David J.
APPLICANT: SAME
FILLE OF INVENTION: NOVEL GPCR-LIKE PROTEINS AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME
FILLE REPERBURG: 21402-022
CURRENT APPLICATION NUMBER: US/09/864,029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA US-09-989-643-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Padigaru, Muralidhara APPLICANT: Spytek, Kimberly A. APPLICANT: Majumder, Kumd APPLICANT: Tchernev, Velizar T. APPLICANT: Tchernev, Velizar T. APPLICANT: Szekeres Jr., Edward S. APPLICANT: Alsobrook II, John P. APPLICANT: Burgess, Catherine E. APPLICANT: Shimkets, Richard A.
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PRIOR APPLICATION NUMBER: 60/206,757
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                  ; Sequence 84, Application US/09989643; Publication No. US20030049636A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Sequence 57, Application US/09864029; Publication No. US20030082174A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
                                     ACAPATGTT 16
1 ACAAATGTT 9
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US20040030110Alel Proteins and Nucleic Acids Encoding Same
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100.0%; Score 9; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
.. OTHER INFORMATION: Description of Artificial Sequence:
.. OTHER OFFICE OFFICE OFFICE PRIMER
US-09-864-029-57
               PRIOR FILING DATE: 2000-07-19

FROR APPLICATION NUMBER: 60/207,020

FRIOR APPLICATION NUMBER: 60/207,020

FRIOR APPLICATION NUMBER: 60/207,020

FRIOR APPLICATION NUMBER: 60/239,542

FRIOR APPLICATION NUMBER: 60/239,542

FRIOR FILING DATE: 2000-01-25

FRIOR FILING DATE: 2000-10-10

FRIOR APPLICATION NUMBER: 60/274,645

FRIOR APPLICATION NUMBER: 60/274,645

FRIOR APPLICATION NUMBER: 60/274,645

FRIOR APPLICATION NUMBER: 60/274,609

FRIOR FILING DATE: 2001-03-09

FRIOR FILING DATE: 2001-03-09

FRIOR FILING DATE: 2001-03-09

FRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PALENTIN VET: 2.1

LENGTH: 22
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Taupier Jr., Raymond J.
Casman, Stacle J.
Ji, Weizhen
Anderson, David W.
PRIOR APPLICATION NUMBER: 60/219,786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles E.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patturajan, Meera
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Vernet, Corine
Zerhusen, Bryan D.
Gorman, Linda
Shenoy, Suresh G.
Pena, Carol E.A.
Smithson, Glennda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MacDougall, John R
Rothenberg, Mark E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu, Ziaohong
Gusev, Vladimir Y
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FILE REFERENCE: 21402-322C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stone, David J
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Sequence 363, Application US/10210130 Publication No. US20040014053A1 GENERAL INFORMATION:
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US-10-032-885-4249/c

US-10-032-885-4249, Application US/10032585

F Sequence 4249, Application US/10032585

Publication No. US2030180953A1

GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Howard, Bussey,
TILLE REPERENCE: 10182-005-999

FILE REPERENCE: 10182-005-999

CURRENT APPLICATION NUMBER: US/10/032,585

CURRENT PILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 8000

SEQ ID NO 4249

LENGTH: 23

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                                      PRIOR APPLICATION NUMBER: 60/281,086
PRIOR PELING DATE: 2001-04-03
PRIOR PELING DATE: 2001-04-03
PRIOR PELING DATE: 2001-04-03
PRIOR PILING DATE: 2001-04-03
PRIOR PILING DATE: 2001-04-05
PRIOR PELING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR PELING DATE: 2001-04-05
PRIOR PELING DATE: 2001-04-10
PRIOR PILING DATE: 2001-04-10
PRIOR PILING DATE: 2001-04-10
PRIOR PELING DATE: 2001-04-13
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100.0%; Score 9; DB 12; I
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 9; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/114,270 CURRENT FILING DATE: 2002-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-032-585-4249
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Best Local Similarity
Matches 9; Conserv
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RESULT 6 US-10-210-130-363/c

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APPLICANT: Taupler, Raymond J., Jr.
APPLICANT: Taupler, Raymond J., Jr.
APPLICANT: Taupler, Raymond J., Jr.
APPLICANT: Statesh G.
ITILE OF INTENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 21402-416C (Cura-716 SMT)
CURRENT PELLING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 05/310,201
PRIOR PLING DATE: 2001-08-02
PRIOR PLING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-08
PRIOR PLING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/313,936
PRIOR PLING DATE: 2001-08-08
PRIOR PRING DATE: 2001-08-08
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 369
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PPLICATION NUMBER: 60/311,979
                                                                                                                                                                                                                                      Li, Li
Bergha, Constance
Zhong, Man
Casman, Stacie J.
Voss, Edward Z.
Boldog, Ferenc L.
Padigaru, Muralidhara
Smithson, Glennda
Ji, Weizhen
Gorman, Linda
Vernet, Corine A.M.
Lieite, Mario W.
Guo, Xiaojia Sasha
Anderson, David W.
Spytek, Kimberly A.
Gerlach, Valerie
Burgess, Catherine E.
Khramtsov, Nikolai V.
APPLICANT: Zerhusen, Bryan D. APPLICANT: Patturajan, Meera APPLICANT: Kekuda, Ramesh APPLICANT: Miller, Charles E. APPLICANT: Rieger, Daniel K. APPLICANT: Pena, Carol E.A. APPLICANT: Shimkets, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DiPippo, Vincent A. Edinger, Shlomit R. Eisen, Andrew J. Gangolli, Esha A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agee, Michele L.
Chaudhuri, Amitabha
Chant, John S.
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Spaderna, Steven K.
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Ellerman, Karen
Rastelli, Luca
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Ooi, Chean Eng
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iu, Xiaohong
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Query Match
Best Local Similarity luv...
9; Conservative
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  ; TYPE: DNA
; ORGANISM: Glycine max
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ORGANISM: Homo sapien
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                                            US-09-969-373-3149
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; Publication No. US2004001414A1
; Publication No. US2004001414A1
; GENERAL INFORMATION;
; APPLICANT: MADSEN, Mogens Winkel
; APPLICANT: FUCKNING, Marianne Scheel
; TITLE OF INVENTION: Method of Screening for Substances Acting on MSK1
; FILE REFERENCE: 3893-0218P
; CURRENT APPLICATION NUMBER: US/10/452,591
; CURRENT APPLICATION NUMBER: PCT/DX00/00505
; PRIOR FILING DATE: 2003-06-03
; PRIOR FILING DATE: 1999-10-13
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 24
                                                                                                                                                                                                                                          Gaps
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                                                                                                                             , OTHER INFORMATION: Description of Artifical Sequence: Primer/Probe US-10-210-130-363
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US-10-452-591-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3149, Application US/09969373
Patent No. US2020133852A1
GENERAL INFORMATION:
APPLICANT: Effetto.
TITLE OF INVANTION: Soybean SSRs and Methods of Genotyping
TITLE OF INVANTION: Soybean SSRs and Methods of Genotyping
FILE REPRENCE: 38 = 10 (5.5679) A
CURRENT PILING DATE: 2001-10-02
PRIOR PELICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR PELICATION NUMBER: US 09/760,427
PRIOR PELICATION NUMBER: US 09/760,427
PRIOR PELICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 3149
                                                                                                                                                                                           Ouery Match
100.0%; Score 9; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Score 9; DB 15; L
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 9; Conservative 0; Mismatches 0;
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 363
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-969-373-3149
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                                                                                                            FEATURE:
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Sequence 8462, Application US/10098263B
Sublication No. US20030104410A1
SUBSET INFORMATION:
APPLICANT: Mitthan, Michael
FILE REFERENCE: 318.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR PELING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
LENGTH: 25
LENGTH: 25
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; Publication No. US20030104410A1
; GENERAL INFORMATION:
    TILE OF INVENTION: Human Microarray
    TILE OF SEPERATION: HUMBER: US/10/098,263B
    CURRENT APPLICATION NUMBER: 60/276,759
    PRIOR PILING DATE: 2001-03-16
    NUMBER OF SEQ ID NOS: 131066
    NUMBER OF SEQ ID NOS: 131066
    SOFWMARE: Microarray Probe Sequence Listing Generator V 1.1
    LENGTH: 25
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100.0%; Score 9; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels
Length 25;
  DB 9; Le
                                                       Mismatches
Query Match 100.0%; Score 9; Best Local Similarity 100.0%; Pred. No. Matches 9; Conservative 0; Mismatch
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US-10-098-263B-15022
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; ORGANISM: Homo sapien
US-10-098-263B-16054
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US-10-098-263B-22881
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US-10-098-263B-22882
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Sequence 16054, Application US/10098263B

Publication No US20030104410A1

GENERAL INRORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REPRENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT FILING DATE: 2003-01-08

FRIOR PEPLICATION NUMBER: 60/276,759

FRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 16054

LENGTH: 25

TYPE: DNA
Sequence 15022, Application US/10098263B
Publication No. US2030104410A1
GENERAL INFORMATION:
APPLICANT: Mitchan, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR PELLING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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Sequence 16053, Application US/10096263B
Sequence 16053, Application US/10096263B
CENERAL INFORMATION: US0030104410A1
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118-1
CURRENT FILING DATE: 2003-01-08
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: Homo sapien
US-10-098-263B-16053
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CORGANISM: Homo sapien
US-10-098-263B-15022
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| Publication No. US20030104410A1
| GENERAL INFORMATION:
| APPLICANT: Mitchean, Michael
| TITLE OF INVENTION: Human Microarray
| FILE REFERENCE: 318.1
| CURRENT APPLICATION WUMBER: US/10/098,263B
| CURRENT FILING DATE: 2003-01-08
| PRIOR FILING DATE: 2001-03-16
| NUMBER OF SEQ ID NOS: 131066
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| LENGTH: 25
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; Publication No. US20030104410A1
; GENERAL INFORMATION:
APPLICANT: Mittnan, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
100.0%; Score 9; DB 14; Length 25; 100.0%; Pred. No. 3.7e+04; ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.7e+04;
Live 0; Mismatches 0;
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  Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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CORGANISM: Homo sapien
US-10-098-263B-22882
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) ORGANISM: Homo sapien
US-10-098-263B-22881
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The present invention describes genetic variants of the human glutathione reductase (GSR) gene (1). (1) has antianaemic activity and can be used in gene therapy. (1) can be used in Screening for drugs targeting (1) that are useful for treating haemolytic anaemia. Methods from the present invention can be used: for improving the efficiency and reliability of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Page 14; 137pp; English.
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Aax72750 Mouse flk
Aax95125 Canine IL-
Aav95126 Canine IL-
Aav94640 Human IL-
Aav94639 Human IL-
Aaf64437 Hammerhea
Aaf64885 Hammerhea
Aaf64885 Hammerhea
Aaf64885 Hammerhea
Acc54403 Human tum
Adb42327 Tumour su
Adb42327 Tumour su
Aab1799 Dihydropy
Aaa57101 Human cad
Ab189242 HIV-1 rel
Ab189240 HIV-1 rel
Ab189251 HIV-1 rel
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                    - nucleic search, using sw model
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AAX72751
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour anglogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAK67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention

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100.0%; Score 9; DB 2; Length 17; 100.0%; Pred. No. 3.2e+04; ive 0; Mismatches 0; Indels

Liarity 100.0%; Conservative 0

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Query Match

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1 ACAAATGTT

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Sequence 17 BP; 5 A; 3 C; 4 G; 0 T; 5 U; 0 Other;

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diseases associated with GSR activity; for haplotyping, which is also used by the pharmaceutical research scientist to validate GSR as candidate target for treating a specific condition or disease predicted to be associated with GSR activity, e.g. haemolytic anaemia, and in the design of clinical trials for treating a specific condition of disease cassociated with GSR activity, e.g. haemolytic anaemia, and in the design of clinical trials for treating a specific condition of disease associated with GSR activity, and for screening compounds targeting GSR.

(I) is useful in studying the expression and function of GSR, and in expressing GSR protein for use in screening for candidate drugs to treat diseases related to GSR activity. (I) is also useful in studying the effect of the variation on the biological activity of GSR as well as on the binding affinity of candidate drugs targeting GSR for the treatment of haemolytic anaemia. The present sequence represents an allele specific cligonucleotide (ASO) primer for the human GSR gene, which is given in the chowing a single nucleotide polymorphic base (showing an IUPAC ambiguity code (as given in the present invention)
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Similarity 100.0%; Pred. No. 3.26+64;
9; Conservative 0; Mismatches
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96US-00584040
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foetal liver kinase 1; ss
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Local Similarity
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11-JAN-1996;
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The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mENA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumcur argiogenesis, coular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
                                                                                                                                                                                                                      Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; KDR; tumour anglogenesis; psoriasis; rheumatoid arthritis; ocular disease; fme-like tyrosine kinase 1; kinase insert domain containing receptor; foetal liver kinase 1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid molecule modulating VEGF receptor(s) gene expression or stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                                                                                                        Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #184
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No. 3.2e+04;
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100.0%; Pred.
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ID AAX72751 standard; RNA; 17
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                                                                                                                                                       (first entry)
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Best Local Similarity
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11-JAN-1996;
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Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.

Claim 4; Page 128; 218pp; English.

Stinchcomb D, Escobedo J;

Pavco P, Mcswiggen J,

WPI; 1997-259017/23

The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VBGF). A patient (preferably human) having a condition associated with the level of the

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The present sequence invention describes ribozymes targeted to modulate the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA. AAV93889 to AAV94574 represent specifically claimed ribozymes, and AAV93675 to AAV95260 represent specifically claimed substrate sequences from the present invention. The ribozymes can be used for the treatment of, e.g. graff rejection, autoimmune disease, cancer, psoriasis, allergy and other inflammatory conditions. The ribozymes are also used to induce tolerance in a recipient to alloantigen from a donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribozymes targetted to interleukin 2 - useful for treating e.g. cancer, autoimmune disease and allergies.
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hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
autoimmune disease; psoriasis; allergy; inflammatory disease;
graft rejection; ss.
                Human, IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
autoimmune disease; psoriasis; allergy; inflammatory disease;
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AAV95126/c
ID AAV95126 standard; RNA; 17 BP.
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9; Conservative
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                                                                                         graft rejection, ss
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                                                                                                                                       Homo sapiens
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Gaps
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  Mismatches
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AAV95125 standard; RNA; 17 BP.
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  9; Conservative
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XX AAV9,
XX DT 24-FI
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AAV9512
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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of enythropoietin, granulocyte colony stimulating factor protein and
and other inflammatory conditions. The ribozymes are also used to induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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                                                                                Length 17;
                  tolerance in a recipient to alloantigen from a donor
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                                                 Sequence 17 BP; 4 A; 4 C; 2 G; 0 T; 7 U; 0 Other;
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100.0%; Pred. No. 3.2e+04;
tive 0; Mismatches 0;
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Best Local Similarity
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ID AAF0488
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                                                                                                                                                                              The present sequence invention describes ribozymes targeted to modulate the synthesis and/or expression of interleukin (II)-2R gamma encoded RNA. AAV93889 to AAV94574 represent specifically claimed ribozymes, and AAV94575 to AAV95260 represent specifically claimed substrate sequences from the present invention. The ribozymes can be used for the treatment off, e.g. graff rejection, autoimmune disease, cancer, psoriasis, allergy and other inflammatory conditions. The ribozymes are also used to induce tolerance in a recipient to alloantigen from a donor
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                                                                                                   Ribozymes targetted to interleukin 2 - useful for treating e.g. cancer, autoimmune disease and allergies.
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AAV94639 standard; RNA; 17 BP.
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                                       Stinchcomb DT, Mcswiggen JA;
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      (RIBO-) RIBOZYME PHARM INC
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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRP-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoletin, granulocyte colony stimulating factor protein and interferon alpha
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                                                                                              Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 6 A; 3 C; 2 G; 6 T; 0 U; 0 Other;
                                        Mcswiggen J;
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                                      Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RIBO-) RIBOZYME PHARM INC.
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            (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                     WPI; 2000-647423/62
                                         Zwick M,
                                                                                                                                                                                                                                                                                                                                                                                                         1 ACAAATGTT
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                                         Blatt L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and
                                                                                                                                                                                                                                                                                                                                                            Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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                                                                                      Ribozyme; erythropoietin; granulocyte colony stimulating factor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 17 BP; 6 A; 3 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                        Mcswiggen J;
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                                                          Hammerhead ribozyme substrate #2400.
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 110; 164pp; English.
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                                                                                                                                                                                                                     11-APR-2000; 2000WO-US009721,
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                                                                                                                                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC.
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                             16-FEB-2001 (first entry)
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                                                                                                  interferon alpha; ss.
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Best Local Similarity
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                                                                                                                                Homo sapiens.
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   AAF04884;
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consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents an isolated nucleic acid sequence associated with tumour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
                                                                                       Gaps
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                                                                                                                                                                                                                                                                          ss; tumour suppressor; antitumour; cytostatic; tumour suppression; tumour regression; apoptosis; virus resistance; diagnosis; cellular degeneration.
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100.0%; Score 9; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                100.0%; Score 9; DB 3; Length 17; 100.0%; Pred. No. 3.2e+04; ative 0; Mismatches 0; Indels
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                                             Sequence 17 BP; 5 A; 3 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                       Human tumour suppressor sequence #3170,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuijnder M, Telerman A, Amson R;
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                                                                                                                                                                                        BP.
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                                                                              Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                             1 ACAAATGTT
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                                                                                                                                                                                                             ACC54403;
                                                                    Query Match
                                                                                                                                                                    RESULT 12
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RESULT 13 ADB42327 ID ADB42327 standard; DNA; 17 BP.

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The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the nucleotides, remained and/or amplifying nucleic acids, as in vitro identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour cupression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and experimental models. The nucleotides (also vectors containing them and call degeneration) (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides can be used for diagnosis and/or prognosis of these diseases. The nucleotides and polypeptides can and/or prognosis of these diseases. The nucleotides and polypeptides can be used to screen for their specific interactive molecules, potentially useful for treating diseases associated with abnormal expression of the nucleotides associated with abnormal
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                                                                                                                                                                 cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
primer; probe; tumour suppression; tumour reversion; apoptosis;
virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
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                                                                                                Tumour suppression/reversion associated nucleotide #2650.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuijnder M;
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(revised)
(first entry)
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                diagnosis.
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ADB44770
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                                          Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 fragments of at least 15 consecutive nucleotides sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 180% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the conclectides, rowers and or properties or the complement, or corresponding RNA, of the conclectides, rowers and or inverse sequences, of nucleotides involved in tumour sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as recombinant polypeptides and or viral resistance, to produce complement models. The nucleotides (also vectors containing them and calls containing the vectors), the encoded polypeptides and antibodies of firal infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides can be used for diagnosis and so be used to screen for their specific interactive molecules, and also be useful for treating diseases associated with abnormal
                                                      cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss; primer; probe; tumour suppression; tumour reversion; apoptosis; virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
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                          Jumour suppression/reversion associated nucleotide #5093.
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Best Local Similarity 100.
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                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-APR-1998
 18-DEC-2003
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                                                                                                     diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting a splicing defect in the di:hydro:pyrimidine dehydrogenase gene - used to identify subjects sensitive to 5-fluorouracil, toxic to individuals with DPD defects.
Human; dihydropyrimidine dehydrogenase; DPD; slicing defect; detection; 5-fluorouracil; cancer; anticancer; uraciluria; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnose DPD-deficiency disorders such as uraciluria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 24; 38pp; English.
                                                                                                                                                                                                                                                                                                                                 97WO-US004269.
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The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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              Submitted (09-SEP-1997) Department Of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
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Submitted (18-FEB-1998) Department Of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Homo sapiens Chromosome 22q13 Cosmid Clone p76e10, complete
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                                                                                                                                                                                                                                                                                                                                                                                                   annotated as STSS and 81,000 SNPS were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                    Protocol: WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 12981/SvImJ, C3H/HeJ, and BALB/CByJ. The WGS reads were placed uniquely on the MGSCV3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were
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Fransson, I. and Dumanski, J.P. A cosmid clone in meningioma deletion region of 22q13
structure of variation in the laboratory mouse genome (6915), 574-578 (2002)
                                                                                                       Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
Research
320 Charles Street, Cambridge, MA 02141, USA
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Pan, H., Lin, S. and Roe, B.A.
A cosmid clone in meningioma deletion region of 22q13
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/strain="CZECHII/Ei"
/db_xref="taxon:10090"
/map="+ 16 27-755 66714317-66715044"
/clone lib="CZECHII/Ei"
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100.0%; Pred. No. 5.8e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                Tel: 6172521477
Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
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Submitted (19-SEP-1997) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
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Submitted (18-FEB-1998) Department Of Chemistry And Blochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Submitted (14-OCT-1998) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
10 (bases 1 to 43738)
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Transson, I. and Dumanski, J.P.
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The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
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The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
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Homo sapiens Cosmid Clone ll119a4 In Meningioma Deletion Region
Unpublished
                                                                                                                                                         AC000034 43738 bp DNA
Homo sapiens Chromosome 22q13 Cosmid Clone
Deletion Region, complete sequence.
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The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Direct Submission
Submitted (21-JAN-1999) Department Of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Submitted (25-AUG-2002) Department Of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Submitted (09-APR-2003) Department Of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Submitted (12-APR-1999) Department Of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
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Submitted (01-JUN-2000) Department Of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
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On Aug 25, 2002 this sequence version replaced gi:4581185.
Because these overlapping clones came from different libraries.
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100.0%; Pred. No. 3.2e+02;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 17; Conservative
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Direct Submission
Submitted (09-APR-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Suract Submission
Submitted (01-SEP-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
67 3019, USA
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Submitted (12-NOV-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Direct Submission
Submitted (01-JUN-2000) Department Of Chemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Submitted (05-NOV-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Submitted (13-NOV-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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On Sep 1, 2002 this sequence version replaced gi:4582474.
Because these overlapping clones came from different libraries.
Location/Qualifiers
1. 43738
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17 (bases 1 to 43738)
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Direct Submission
Submitted (07-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 53108, USA
4 (bases 1 to 44532)
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                                                                                                                                                                                                                                                                                                                                                                Bukaryotti. Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.

1. (bases 1 to 44532)
Sulston, J. E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                      44532 bp DNA linear PRI 30-MA
Homo sapiens BAC clone RP11-1226B8 from 4, complete sequence.
AC109830
HTG.
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Center code: WUGSC
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Scott, K. and Haglund, K.
The sequence of Homo sapiens BAC clone RP11-1226B8
1 (pubblished (2001)
3 (bases 1 to 44532)
Waterston, R.H.
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Direct Submission
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NOTICE: This sequence may not represent the entire insert of this forbe. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions. This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

USA

Louis,

MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John

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Gaps

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0; Indels

0; Mismatches

100.0%; Score 17; DB 9; Length 43738; 100.0%; Pred. No. 3.2e+02;

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PRI 28-DEC-2001
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6615_ .26806

'note=match to BST B1458889 (NID:g15249545)"

7142. .27187

'rpt_family="AT_rich"

7756_ .29801

9779_ .29801
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4594. .24960
Incle="match to EST BI458889 (NID:g15249545)"
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100.0%; Score 17; DB 9; I
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0;
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30128. .30184
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/rpt_family="L1"
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rpt_family="L2"
1612. .21887
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McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                       SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                      NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is AC015631, 2000 bp overlap; the clone sequenced to the right is RP11-400D2, 2000 bp overlap.
Actual end is at base position 85524 of RP11-400D2.
Location/Qualifiers
                                                                                                                                                                                                                                                                              1. 44532
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1274. 1319
/rpt_family="(TCTA)n"
1428. 1478
/rpt_family="AT_rich"
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/clone lib="RPCI-11"
63. 142
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939. .8944
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rpt_family="AT_rich"
1519. .11638
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1418, .4648
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/rpt_family="MIR"
3322. .5350
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'758. .1280.
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.8954. .19004
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rpt_family="ERVL"
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rpt_family="MIR".
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/rpt_family="AT_ri.
5400. .5483
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/rpt_family="L1"
9538. . a = 7
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5884. .6983
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7909
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18096, 1812-
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1820. 1990.
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family="L1"
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Only the 90.5 kb of the T7 end of this project is being submitted.
The remainder overlaps AC005697 [WICGR project L418].
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complement(463. .760)
/rpc_family="Alusg"
complement(875. .1099)
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complement(12099, .12100)
/rpt_family="Alusp"
                                                                                                                                                                                    family="Alusg"
ement(11451)
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complement(8134. .8224)
/rpt family="MIR"
8288. .8310
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/rpt_family="MIR"
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125. .7571
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__.280A
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complement (5121. .5212)
/rpt_family="MIR"
5186. .6496
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352. ,222
Center project name: L12518
Center clone name: 218_F_4
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complement(7572. .78
                                                                                                                                                             Location/Qualifiers
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family="MLT1A1"
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omplement(4672. .4
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026_ .5081
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:omplement(11146.
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Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 90543)

S birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bognalavkiy, L., Boukigalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Garnd-Pierre, N., Hagos, B., Hadford, A., Karatas, A., Kalls, C., Lacoque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., Macdonald, P., Major, J., Matchews, C., Macdonald, P., Major, J., Matchews, C., Macdonald, P., Major, J., Marchews, C., Macdonald, P., Major, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Donnell, P., O'Norman, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Santos, K., Travers, M., Travis, N., Travis, N., Travis, N., Travers, M., Submission, Direct Submission,
Direct Submission
                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Campoplano, A., Cohepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Golge, S., Farro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Dodge, S., Farro, S., Ferreira, P., FitzHugh, W., Gawe, D., Galagan, J., Gardel, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Lavine, K., Liu, G., MacLean, C., MacCean, K., McCerran, K., McCarthy, M., McCearth, M., Maylor, J., Nguyen, C., Norbu, C., Norbu, C., Norbu, C., Norbu, M., K., Kley, R., Riee, C., Rogov, P., Roman, C., Retta, R., Schauer, S., Schauer, A., Schauer, A., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., 
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90543)
     Homo sapiens chromosome 17, clone RP11-218F4, complete sequence
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                                                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C. and Lander, B. Homo sapiens chromosome 17, clone RP11-218F4 Unpublished
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Web site: http://www-seg.wi.mit.edu
                             AC090287.9 GI:17985917
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                                                                                                              Homo sapiens (human)
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Consensus quality: 83951 bases at least Q40
Consensus quality: 91885 bases at least Q30
Consensus quality: 91885 bases at least Q30
Consensus quality: 91885 bases at least Q30
Consensus quality: 91865 bases at least Q30
Estimated insert size: 97716; sum-of-contigs estimation
Estimated insert size: 97716; sum-of-contigs estimation
Quality coverage: 10.11 in Q20 bases; agarose-fp estimation
Quality coverage: 13.24 in Q20 bases; sum-of-contigg estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                   Unpublished
2 (bases 1 to 100116)
DOE Joint Genome Institute.
Direct Submission
Submitted (15-JUL-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I Chases I to 10116)
DOE Joint Genome Institute.
Sequencing of Mouse
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5: gap of unknown length
2: gap of unknown length
10: contig of 1077 bp in length
10: contig of 1098 bp in length
10: gap of unknown length
11: contig of 1321 bp in length
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Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Center clone name: RPCI-23_77J9
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complement(18030. 18868)
/rpt_family="MRE63"
18236. 18245
/note="430 qual SNGL region."
/note="430 qual SNGL region."
/note="430 qual SNGL region."
/rpt_family="MITIA2"
18965. 18977
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complement (19291. 19390)
/rpt family="WER63"
complement (20076. .20167)
/rpt family="MIR3"
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notce="<30 qual SNGL region."
7837. .17887
rpt_family="Aluyb8"
7874. .17939
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/rpt family="AluJb"

complement (15892. 15899)

//note=="430 qual SNGL region."

16045. 16334
                                                                / Two family = 12557)
/rpt_family="MER103"
complement (12558. 12820)
/rpt_family="Aluy"
complement (1281. 12924)
/rpt_family="MRR103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="MER5A"
7745. .1775.
                    /rpt_family="(ATTTG)n"
complement(12134..12212)
/rpt_family="FLAM"
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4326. .14360
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rpt family="Charlie4a"
(6870 . 17112
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/rpt_family="AT_rich"
| 4689. 15341
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ACO74171 GI:9211281
HTG: HTGS_PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                          rpt_family="MLT1L"
5735. .16044
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5507, .1572/
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20605. .20915
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/gene="dJ1007616.4"
/note="dJ1007616.4 (heat shock 60kD protein 1 (chaperonin)
(HSPD1) pseudogene)
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further
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15334. .21667
note="LIPR2 repeat: matches 4. .6144 of consensus"
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24369. .24451
/note="L2 repeat: matches 2100. .2181 of consensus"
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'note="L2 repeat: matches 1353. .1525 of consensus"
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//note="MIR repeat: matches 51. .203 of consensus"
4304. 4408
/note="L2 repeat: matches 2625. .2748 of consensus"
44433. 4570
/note="MIR repeat: matches 91. .222 of consensus"
5459. .5597
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"note="MIR repeat: matches 27. .183 of consensus"
2067. .2200
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15414. .15533
http://www.sanger.ac.uk/HGP/Chr1
RP5-1007G16 is from the library RPCI-5 constructed at the last Cancer Institute by the group of Pieter de Jong. For details see http://bacpac.med.buffalo.edu/
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                                                                                                                                   This sequence is the entire insert of clone RP5-1007G16.
Location/Qualifiers
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note="LIMC4 repeat: matches 7894. .7977 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note≈"11 copies 2 mer aa 100% conserved"
1653. .7772
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/note="33 copies 2 mer aa 75% conserved"
21737. .23024
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/note=="L2 repeat: matches 2655.
complement (3188. 3624)
/note=="match: GSS: Em:AQ235526"
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6579. .6600
                                                                                                                                                                                                                                                                                                                     /map="p34.2-35.3"
/clone="RE5-1007G16"
/clone lib="RPC1-5"
64. 647
/note="L2_repeat: matches 373.
                                                                                                                                                                                                                organism="Homo sapiens"
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This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as comparessions and repeats, but not necessarily within known sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL, 9w., SWISSPROT; Tr., TREMBL, Wp., WORMPEP, Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger. Centre Chromosome 1 Mapping Group. Further information can be found at
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Hbuman DNA sequence from clone RP5-1007G16 on chromosome
1p34.2-35.3. Contains part of the gene for a novel CUB and Sushi
(SCR repeat) domain protein, a novel high-mobility group
(nonhistone chromosomal) protein 2 (HMG2) like protein (pseudo)
gene, a heat shock 60kD protein 1 (chaperonin) (HSPD1) pseudogene,
ESTS, STSs and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 130604)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 17; DB 2; Length 100116; 100.0%; Pred. No. 2.8e+02;
  55414: gap of unknown length
6415 64486: contig of 9072 bp in length
64286: gap of unknown length
70766: contig of 6180 bp in length
7077 70866: gap of unknown length
7077 76678: contig of 5812 bp in length
679 76778: gap of unknown length
7078: gontig of 5808 bp in length
7078: gap of unknown length
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HTG; chaperonin, CUB; HWG2; HSP60; HSPD1; Sushi.
HOmo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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/clone="RP3-7739"
/clone_lib="RPCI mouse BAC library 23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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COMMENT

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DOE Joint Genome Institute.

DOE Joint Genome Institute.

Direct Submission

Submitted (03-406-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 135331)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www-shgc.stanford.edu
duality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
NOTS: This insert is not the entire sequence of the clone. It is clipped at the overlap with AC008507. The number of bases overlapped is 46781.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 135331)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Unpublished
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Submitted (19-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

4 (Dases 1 to 135331)

DOE Joint Genome Institute and Stanford Human Genome Center.
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                                        AC008798 135331 bp DNA linear PRI 12-JUL-
Homo sapiens chromosome 19 clone CTD-2057D4, complete sequence.
AC008798
    'note="MIR repeat: matches 3. .118 of consensus"
                                                                                                                                                                                                                                                                                                                       Length 130604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 17; DB 9; Length 135331;
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100.0%; Pred. No. 2.7e+02;
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/db_xref="taxon:9606"
/chromosome="19"
/clone="CTD-2057D4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        97118 rerecaaceaaraara 97134
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Homo sapiens
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Best Local Similarity 100.0
Matches 17; Conservative
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AC008798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  match: proteins: Tr:060494 Tr:Q9TU53 Sw:P13497 Tr:Q9Z135 Tr:043897 Tr:Q9X561 Sw:P98069 Tr:Q9UQ00 Sw:Q15113 Sw:Q61389 Tr:Q44072 Tr:Q9X6L7 Tr:057381 Tr:057382 Tr:Q9WVM6 Sw:008628 Tr:Q91925 Tr:Q62381"
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5660. .35774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28558. .28868
/note="MER58B repeat: matches 23. .337 of consensus"
29639. .29709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hote="LTR33 repeat: matches 44. .119 of consensus"
29715. .30122
hote="LTR33 repeat: matches 102. .517 of consensus"
80214. .30320
hote="MRR20 repeat: matches 2. .102 of consensus"
90357. .30478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="exon boders derived from FGENESH and GENSCAN predictions; true borders could be further down- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=2
/codon_start=2
/produce=not experimental
/produce==dal007416.3 (novel CUB domain protein)"
/protein_id="CAC05319.1"
/bb_xref="G1:12314082"
/db_xref==G1:123140802"
/tb_xref==G1==PTGASLPAPVISSKWMLRLHFTSDGNHRQRGFSAQYQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                note="12 repeat: matches 2362. .2529 of consensus" 7969. .28555 note="12 repeat: matches 1685. .2333 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MER20 repeat: matches 98. .218 of consensus"
0592. .30802
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35903. .36201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4160. .34582
"note="LTR33 repeat: matches 1. .450 of consensus"
15326. .35657
Sw:033963 Sw:Q05045 Tr:097480 Sw:Q95058 Tr:097131 Sw:P77829 Sw:Q9ZCT7 Sw:Q85754 Sw:P49464 Tr:Q51919 Sw:P95578 Sw:Q94596 Sw:G6024 Tr:P90662 Sw:G034198 Sw:P51349 Sw:P37282 Sw:P35861 Sw:P35862 Sw:Q05972 Tr:P993570"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 1. .216 of consensus" 31220. .31393
/note="MIR repeat: matches 56. .226 of consensus" 22452. .32652. .32652
/note="MIR repeat: matches 2. .261 of consensus" complement(join(32897. .33009,104107. .104314))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MIR repeat: matches 76. .247 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MIR repeat: matches 29. .251 of 3764, .33933
                                                                                                                                                              /evidence=not_experimental
complement(24669, .25200)
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complement(25663. .26219)
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                                                                                                                                                                                                                                               /note="match: GSS: Em:AQ309682"
26085. .26326
                                                                                                                                                                                                                                                                                                                                                                  26106. ,26574
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complement (<32897. .>33009)
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RESULT 9 AC079112/c LOCUS

SOURCE ORGANISM

VERSION KEYWORDS ACCESSION

REFERENCE AUTHORS

TITLE JOURNAL MEDLINE PUBMED

REFERENCE AUTHORS TITLE JOURNAL REFERENCE

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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P. Y., Zhao, B., Frengen, E. Tateno.M., Catanese, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bapapc.med.buffalo.edu)
NECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                      The clone sequenced to the left is RPI1-30P5; the clone sequenced to the right is RPI1-474G23. Actual start of this clone is at base position I of RPI1-67K11; actual end is at base position 155888 of RPI1-67K11.
         sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .155888
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/rpt_family="ERV1"
2082. .2215
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/rpt_family="ERV1"
2390. .2801
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/rpt_family="Alu"
5603. .590^
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1746. .3978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     />85. .7708
/rpt_family="Alu"
/709. .7824
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5993. .7584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="AT_ri.
10172. .10432
/rpt_family="Alu"
10433. .10741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12910. .13181
/rpt_family="Alu"
13182. .13483
/rpt_family="Alu"
13749. .14156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        825. .7905
rpt_family="Malk"
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1491. .11646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'rpt_family="MaLR"
7825. .7905
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2219. 2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="MIR"
4181. .4281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="MIR"
1536. .4849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="MIR"
2515. 12833
rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="L1"
0088. .10108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'rpt_fa
2910.
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Center: Washington University Genome Sequencing Center Center Conter Conter code: WUGSC

Web site: http://genome.wustl.edu/gsc
Context: sapiens@wastson.wustl.edu
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Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-MAY-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.

1. (bases 1 to 155888)

Sulston, J.E. and Waterston, R.

Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                             Gape
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4444 Forest Park Parkway, St.
                                                                                                                                                                                                            ACU/9112 155888 bp DNA linear PRI 07-N
Homo sapiens BAC clone RP11-67K11 from 2, complete sequence.
AC079112
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Goyae,E., Mishra,S. and Kozlowicz,A.
The sequence of Homo sapiens BAC clone RP11-67K11
Unpublished
                                Indels
100.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: H_NH0067K11
                             Mismatches
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Submitted (18-AUG-2000) Genome
University School of Medicine,
MO 63108, USA
                                                                                                   TGTGGAAGGAATAAATA 82062
                                                                                                                                                                                                                                                                                    AC079112.4 GI:14091934
                                                                  1 TGTGGAAGGAATAAATA 17
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Waterston, R.H.
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Waterston, R.H.
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Matches 17; Conserv
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AUTHORS TITLE JOURNAL

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COMMENT

REFERENCE AUTHORS

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2. (bases 1 to 155165)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Bouklagalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Firzhugh, W., Forrest, C., Galego, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Haeford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Lui, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McCurk, A., McKernan, K., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pisani, C., Follars, V., Raymond, C., Riley, R., Rothman, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Direct Submission and Street, Cambridge, MA, 02141, USA, On Apr. 1, 2000 this sequence version replaced gi: 6721267.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
              AC021453 156165 bp DNA linear HTG 01-APR-2000
Homo sapiens clone RP11-125C16, WORKING DRAFT SEQUENCE, 14
                                                                                                                                                                                                Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 156165)
Birren, B., Linton, L., Musbaum, C. and Lander, E.
Homo sapiens, clone RP11-125C16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence submissions@genome.wi.mit.edu
Contact sequence submissions@genome.wi.mit.edu
Contact project Information
Center project name: 125 C 16
Center clone name: 125 C 16
Center clone name: 125 C 16
Center clone name: 125 C 16
Consending vector: M13, M77815, 100% of reads
Assembly program: Phrap, version 0.960731
Consensus quality: 15104 bases at least 040
Consensus quality: 15104 bases at least 030
Consensus quality: 153345 bases at least 020
Insert size: 160000; agarose-fp
Insert size: 164865; aum-of-contigs
Quality coverage: 4.1 in 020 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                                                                                                    HTG; HTGS PHASE1; HTGS DRAFT.
Homo sapiens (human)
Homo sapiens
                                                                                                    AC021453.3 GI:7382318
                                                                                                                                                                                                                                                                                                                        (bases 1 to 156165)
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  RESULT 10
AC021453
LOCUS
DEFINITION
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26789. .27175
/rpt_family="MalR"
27258. .27303
                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="MER1_type"
1829. .22040
rpt_family="MIR"
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rpt_family="AT_rich"
5479. .25657
                                                                                                                                                                                                                                                            family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                               . .20179
family="CT-rich"
                                                                                                                                                                                                                        family="GA-rich"
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/rpt_family="(CA)n"
30417. .30cc
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/rpt_family="(CA)n"
27536. .27604
/rpt_ly="MIR"
27589. .27627
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/rpt_family="ERVL"
31120, .31275
                                                                                                                                                                                                                                                                                                     ly=" (TC) n"
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  B. .14654
family="MaLR"
3. .14928
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25658 .25929
/rpt_family="Alu"
25930 .2600
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/rpt_family="L1"
23117. .23428
/rpt_family="Alu"
                                                           family="Malk"
                                                                                                rpt_family="MaLR"
5940. .17923
                                                                                                           15940. 17923
/rpt_family="L1"
| 18057. 18200
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rpt_family="L1"
2757.
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6390. .26739
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8276. .28369
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rpt family="L2"
6003. 26168
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pt_family="L1"
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9950. .30197
                                                           rpt_family="N
4990. .15229
                                                                                                                                                                                                                                                                                                                                                                                                       .21686
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8806.
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. 1836: contig of 1836 bp in length 1936: gap of 100 bp 5796: contig of 3860 bp in length 1837

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Gaps

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126218 TGTGGAAGGAATAATA 126202

1 TGTGGAAGGAATAATA 17

PRI 29-AUG-2002

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 157980)
                                                              AC100852 157980 bp DNA linear PRI 29-AUG-20
Homo sapiens chromosome 17, clone RP11-125C16, complete sequence.
AC100852
                                                                                                                                                                                                                                                                                                                         Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone RP11-125C16
                                                                                                                                                    AC100852.2 GI:22539166
HTG.
                                                                                                                                                                                                 Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                 RESULT 11
AC100852
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5896: gap of 100 bp 9997: contig of 3901 bp in length 9897: contig of 402 bp in length 19819: contig of 402 bp in length 14019: gap of 100 bp 17500: gap of 100 bp 21550: gap of 100 bp 21553: gap of 100 bp 21553: contig of 3753 bp in length 31096: contig of 9743 bp in length 31096: gap of 100 bp 41665: contig of 100 bp 50001: contig of 10269 bp in length 41565: gap of 100 bp 50001: contig of 10269 bp in length 51001: gap of 100 bp 50001: gap of 100 bp 62141: gap of 100 bp 75247: contig of 1360 bp in length 75347: gap of 100 bp 100 bp 1000 bp
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Matches 17; Conserv
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(EE 2 (bases 1 to 157980)

Richard, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Callins, S., Collymore, A., Cock, P., Colangelo, M., Callins, S., Collymore, A., Cock, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S. Ferreira, P., FitzHugh, W., Gagedan, J., Garad-Pierre, N., Glode, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Marquis, N., Mathews, C., MacCarthy, M., McEwan, P., McKernan, K., McPheeters, M. Mathews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Melli, D., Olonnell, P., O'Norman, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Norman, C. H., O'Connor, T., O'Donnell, P., O'Norman, C. M., Roy, A., Santos, R., Schauter, S., Schupback, R., Santos, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauter, S., Schupback, R., Statuss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Myman, D., Ye, W.J., Young, G., Subhitted, Submission, M., Tarvis, N., Trigillo, J., Ye, W.J., Young, G., Submitted, C., Morder, M., Whitter, J., Lamar, A., Myman, D., Ye, W.J., Young, G., Submitted, C., Morder, M., Whitter, J., Jamer, A., Wassiliev, H., Viel, R., Wassiliev, H., Wassiliev, H., Submitted, C., Martin, M., M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., M., Martin, M., Marti
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Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

E 3 (Dases 1 to 157980)

Birren, B., Nubbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cook, A., Perreira, P., Fitzaro, B., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Gord, S., Graham, L., Grand-Pierre, N., Hagsn, J., Hulme, W., Iliev, I.., Johnson, R., Lindblad-Toh, K., Lindblad, K., Karles, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, M., Macdonald, P., Major, J., Matthews, C., McCarth, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., McCarth, M., Naylor, J., Manor, T., Mhora, T., Mererson, K., Comman, C., Norman, C., Norman, C., Phunkhang, P., Pierre, N., Rangell, P., O'Neil, D., Ollver, J., Pererson, K., Schauer, S., Schauer, M., Vassiliev, H., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Virent, S., Voll, K., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Priester, S., Ander, A., Wu, X., Wyman, D., Young, G., Zainoun, J., Richel, R., Vol, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Richer, S., Rander, A., and Zody, M.
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Center: Whitehead Institute/ MIT Center for Genome Research
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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Gaps

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Conservative

repeat_region

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AC024563 158541 bp DNA linear PRI 14-JUL-2002
HOMO sapiens chromosome 19 clone CTC-451A6, complete sequence.
AC024563.6 GI:21747460
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100.0%; Score 17; DB 9; Length 157980;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0;
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                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 15841)

2 DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

1 Unpublished

2 (bases 1 to 158541)

2 Doe Joint Genome Institute.

Direct Submission

Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

E 3 (bases 1 to 15844)

S DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens chromosome 16 clone RP11-46309, complete sequence. AC009108
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1 (bases 1 to 168656)

DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission
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Submitted (01-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell
Submitted (01-SEP-2000) DOE Joint Genome Center.

(1) Chases 1 to 158541)

DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (03-0CT-2001) DOE Joint Genome Institute, 2800 Mitchell
Submitted (03-0CT-2001) DOE Joint Genome Institute, 2800 Mitchell
Dirve, Walnut Creek, CA 94598, USA
(Dasses 1 to 158541)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (14-U12.2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jul 14, 2002 this sequence version replaced gi:15887308.
Draft Sequence Produced by DOE Joint Genome Institute
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Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.7.

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/db_xref="taxon:9606"
/chromosome="19"
/clone="CTC-451A6"
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Direct Submission

AL Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 16926)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastlen, V., Bloom, T., Bouklay, L., Boukhagaler, B., Chang, U., Charagi, E., Choepel, Y., Collymore, A., Cook, P., Coke, P., Chang, U., Chang, U., Chang, U., Chang, U., Chang, U., Chang, U., Ganarata, J., Candra, S., Cardian, L., Grand, P., Galgan, J., Farcoin, E., Hulme, W., Illev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad, Toh, K., Liu, G., Macdonald, P., Major, J., Matthews, C., Landers, T., Major, J., Matthews, C., Landers, L., Milo, W., Lindblad, Toh, K., Lindblad, Toh, K., McZartas, R., Major, J., Matthews, C., Landers, L., Major, J., Matthews, C., Rogov, P., Phunkhang, P., Pierre, N., Nguyen, C., Nicol, R., Norba, C., Regov, P., Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Seange-Thomann, N., Stojanovic, N., Talamas, J., Vel, R., Vo, A., Wilse, T., Topham, K., Travers, M., Vassiliev, H., Zimmer, A. and Zody, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON AUG 11, 2002 this sequence version replaced gi:20163106. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research Center: Whitehead Institute/ MIT Center for Genome Research WIBM with the site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu Center project name: 119818 Center clone name: 177_0_15
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Direct Submission
Submitted (08-WAR-2000) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA
Of Washington, PO BOX 357730, Seattle, WA 98195, USA
Submitted, Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Nesbitt, R., Traicoff, R. and Hood, L. Harrison, G., Kaur, A., Madan, A., Direct Submission
Submitted (03-FBB-2001) Multimegabase Sequencing Center, Institute
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Homo sapiens chromosome 15 clone RP11-548M13 map 15q21.3, complete
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[ (bases 1 to 170749)

Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A., Madan,A., Sequencing of human chromosome 15 D15S146-D15S117 region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., James, R., Kaur, A., Madan, A., Owen, M.P., Ratcliffe, A., Shaffer, T. and Hood, L.
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On Feb 3, 2001 this sequence version replaced gi:8272670.
Conter: Multimagbase Sequencing Center
Center: Multimagbase Sequencing Center
Center code: UMNSC
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowen@systemsbiology.org
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Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
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vector_side:right"
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AAK80495 ACF62730 ADB20845

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ADB60638

Human mus

Human imm Human int Polymorph Nucleotid

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abk48984 Genomic D	Aak73688 Human imm	Aak73689 Human imm	Aak58790 Human imm	Aat74041 Soybean t	Aak73690 Human imm	Aak73691 Human imm	Aal07315 Human rep	Aba08182 Human ova	Abz01147 Human leu	Aat20169 Human gen	Add17249 DNA (SeqI	Add17846 DNA (SeqI	н	Aah31558 Human olf	Aas90796 DNA encod	Aac59279 Human sec	Aah33029 Human col	Abg81553 Gene up-r	u	Drosc	a	Abz57733 Human hea
SUMMARIES	ID	ABK48984	AAK73688	AAK73689	AAK58790	AAT74041	AAK73690	AAK73691	AAL07315	ABA08182	ABZ01147	AAT20169	ADD17249	ADD17846	ADD16351	AAH31558	AAS90796	AAC59279	AAH33029	ABQ81553	ABQ81555	ABL05143	ABL26332	ABZ57733
	DB	6	4	4	4	N	4	4	4	4	9	~	Φ	Q	σ	4	'n	٣	4	9	ø	4	4	9
	Length	6458	405	406	418	1807	9124	21619	21619	21619	50	215	601	601	602	657	943	1140	1555	1780	2336	33	2755	3022
. *	ery	100.0	94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.1	ö	ö	О	0	0	90.6	90.6	ö	ö	90.6	ö	ö	•	ö
	Score	17	16	16	16	16	16	16	16	16	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4
	Result No.		0	ი ი	Ω 4	ហ	9 U	0	B U	ص ن	10	11	12	13	14	15	c 16	17	18	19	20	21	22	. 23

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Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                               Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28500.
              Gaps
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0
    Pred. No. 1.3e+02;
; Mismatches 0; Indels
100.0%; Pr
                                                                                  RESULT 2
AAK73688/c
ID AAK73688 standard; DNA; 405 BP
                                                   359 rdrddaaddaaraara 375
                                  1 TGTGGAAGGAATAATA 17
                                                                                                                                                                                                                                                                           17-JAN-2001; 2001WO-US001354
                                                                                                                                             (first entry)
    Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                    WO200157182-A2
                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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14-AUG-2000;
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                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                         AAK73688;
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                                                   OP
                                                                                                                         /*tag= 1
/note= "Fragment of the FOXC2 promoter. Specifically
claimed in claim 1"
1746. .4629
/*tag= n
/note= "First exon according to the published form of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes an isolated human FOXC2 promoter region. The mammalian FOXC2 promoter region for the modulation of FOXC2 polypeptide expression has therapeutic value in treating type II diabetes mellitus, obesity, hypercholasterolaemia, other cardiovascular diseases or dyslipidaemias. This sequence encodes the human transcription factor FOXC2, the promoter of which is described in the invention
            /*tag= i
/*tag= i
/note= "Fragment of the POXC2 enhancer. Specifically
claimed in claim 15"
/*tag= k
/*tag= k
/note= "Fragment of the POXC2 promoter. Specifically
claimed in claim 3"
/*tag= j
/note= "Fragment of the FOXC2 promoter. Specifically
claimed in claim 2"
claimed in claim 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An isolated FOXC2 promoter region that modulates the expression of a FOXC2 polypeptide is useful for treating obesity and type II diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                              /*tag= q /note= "Portion of polypeptide used in alternative rranscript" 7741. 4629 /*tag= s
                                                                                                                                                                                                                                                                                                          *tag= r
'note= "Second exon according to the alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6458 BP; 1443 A; 1826 C; 1715 G; 1474 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                             *tag= p
note= "Region coding for DNA-binding domain"
1516, .4629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wasserman WW;
                                                                                                                                                                                                                                                         note= "Transcription factor'
448. .2735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 33-38; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rondahl L,
                                                                                                                                                                                                                                              product= "FOXC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-SEP-2000; 2000SE-00003435.
10-OCT-2000; 2000US-0238897P.
09-NOV-2000; 2000SE-00004102.
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2516. .3740
                                                                                                                                                                                               ranscript"
     .423
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     misc_difference 403.
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P-PSDB; AAU79816.
                                                                                 misc_difference
                                                                                                                         misc_difference
                                           misc_difference
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                                                                                                                                                                                                                                                                                                                                    misc_feature
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2000US-0230438P

06-SEP-2000;

100.0%; Score.17; DB 6; Length 6458;

Query Match

17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

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2000US-0232398P
              000US-0240960P
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) and a deguences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For exament of diseases associated with inappropriate (1) expression. For expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polymucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polymucleotides may be used to produce the secreted (1), by inserting the diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells, AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic represent sequences from the present invention. AAK64942 to AAK54950 and AAM82169 represent invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, immune, haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 28500; 3071pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 405 BP; 126 A; 73 C; 50 G; 156 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA, Barash SC, Ruben SM
                                                                  2000US-0249299P.
2000US-024930P.
2000US-0250160P.
2000US-0251030P.
2000US-025198BP.
2000US-025198BP.
2000US-025149P.
2000US-025149P.
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2000US-0251869P.
2000US-0251989P.
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                                                                                                                                                                                                                                                                                                                        05-JAN-2001; 2001US-0259678P
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17-NOV-2000)
01-DEC-2000)
05-DEC-2000)
05-DEC-2000)
05-DEC-2000)
06-DEC-2000)
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 31-JAN-2000; 2000US-0179065P-04-FEB-2000; 2000US-0180628P-24-FEB-2000; 2000US-0180628P-02-MAR-2000; 2000US-0180628P-02-MAR-2000; 2000US-0180874P-02-MAR-2000; 2000US-0180874P-02-MAR-2000; 2000US-0180874P-02-MAR-2000; 2000US-0198074P-02-MAR-2000; 2000US-0198074P-02-MAR-2000; 2000US-0198074P-02-MAR-2000; 2000US-0198074P-02-MAR-2000; 2000US-0198074P-02-MAR-2000; 2000US-0198074P-02-MAR-2000; 2000US-0198064P-02-MAR-2000; 2000US-0114806P-02-MAR-2000; 2000US-0114447P-02-MAR-2000; 2000US-011444P-02-MAR-2000; 2000US-011444
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                            WO200157182-A2
Homo sapiens
                                                                                     17-JAN-2001;
                                                         09-AUG-2001
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14-AUG-2000;
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30-AUG-2000;
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01-SBP-2000

01-SBP-2000

05-SBP-2000

05-SBP-2000

06-SBP-2000

06-SBP-2000

08-SBP-2000

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08-SBP-2000

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08-SBP-2000

08-SBP-2000

08-SBP-2000

08-SBP-2000
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26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
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12-SEP-2000
14-SEP-2000
  AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (1)
proteins and polyunclectides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (1) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (1) by expressing inactive proteins or to
supplement the patients own production of (1). Additionally, (1)
polynucleotides may be used to produce the secreted (1), by inserting the
nucleic acids into a host cell and culturing the cell to express the
chack and treat immune/haematopoietic-related diseases, especially
concers and cancer metastases of haematopoietic-derived cells, AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK45492 to AAK5450 and AAM82169
represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                            ö
                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3850.
                                                                                     Disclosure; SEQ ID NO 28501; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                   94.1%; Score 16; DB 4; Length 406; 100.0%; Pred. No. 3.4e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                               Seguence 406 BP; 126 A; 74 C; 50 G; 156 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA, Barash SC, Ruben SM
                                                                                                                                                                                                                                                                                                                                                                                                     rGrecahchahah 347
                                                                                                                                                                                                                                                                                                                                                                                TGTGGAAGGAATAAAT 16
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Best Local Similarity 100..
Best Local Similarity
Local Similarity
                                WPI; 2001-483426/52.
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20-OCT-2000; 2000US-0241826P.
01-NOV-2000; 2000US-0244617P.
08-NOV-2000; 2000US-0246475P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246477P.
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08-NOV-2000; 2000US-0246528P.
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17-NOV-2000; 2000US-0249214P.
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(HUMA-) HUMAN GENOME SCI INC

Ruben SM; Barash SC, Rosen CA,

WPI; 2001-483426/52 P-PSDB; AAM86009 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Claim 1; SEQ ID NO 3850; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91291. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and tracament of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the

Sequence 1807 BP; 500 A; 387 C; 449 G; 471 T; 0 U; 0 Other;

Length 1807;

5

Score 16;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a novel thiol protease D3-alpha derived from germinated soybean cotyledon. A method for the production of thiol protease using Escherichia coli transformed with recombinant expression vectors containing a DNA sequence encoding thiol protease has been produced. The method can be used to prepare large amounts of thiol protease with high efficiency
nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK8464 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK64942 to AAK84950 and AAW82169 represent sequences used in the exemplification of the present invention
                                                                                                                                                                     Gaps
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0
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                                                                                                                                        Length 418;
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                                                                                                              Sequence 418 BP; 124 A; 77 C; 55 G; 157 T; 0 U; 5 Other;
                                                                                                                                        94.1%; Score 16; DB 4; Le
100.0%; Pred. No. 3.4e+02;
tive 0; Mismatches 0;
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/product= "Thiol_protease"
68. .460
                                                                                                                                                                                                                                                                                                   AAT74041 standard; cDNA to mRNA; 1807 BP.
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461. .1459
/*tag= c
/product= "D3-alpha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                            371 TGTGGAAGGAATAAT 356
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95JP-00245279.
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Best Local Similarity 100.0
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-DEC-1994;
30-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                recombinant
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22-OCT-2000

02-OCT-2000

13-OCT-2000

13-OCT-2000

13-OCT-2000

20-OCT-2000

20-OC
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                            Gaps
                                                                                                                                                                                                                                                                                                                                     Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28502
                            ô
                          Indels
    Pred. No. 3.8e+02; ; Mismatches 0;
                                                                                                                                                          Best Local Similarity 100.0%; F
Matches 16; Conservative 0;
                                                                                                See GTGGAAGGAATAAATA S81
                                                             2 GIGGAAGGAAIAATA 17
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2000US-0229287P.
2000US-0229343P.
2000US-0229344P.
2000US-0229345P.
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2000US-0231413P.
2000US-0231414P.
2000US-0232080P.
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2000US-0232081P.
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2000US-0191076P.
2000US-0191076P.
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2000US-0232398P.
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                                                                                                    17-JAN-2001; 2001WO-US001354
                                     WO200157182-A2
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22-AUG-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                 28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
     Homo sapiens.
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                                                                   09-AUG-2001
   88\%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polyuncleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting the
cucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK64992 to AAK64900 and AAM82169
represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, immune, haematopoietic, immune/haematopoietic antigen, cancer, cytostatic, gene therapy, vaccine, metastasis, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 28502; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9124 BP; 3077 A; 1494 C; 1554 G; 2999 T; 0 U; 0 Other;
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100.0%; Pred. No. 4.2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Barash SC, Ruben SM,
17-NOV-2000, 2000US-0249245P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249300P.
17-NOV-2000; 2000US-0249300P.
17-NOV-2000; 2000US-02599P.
17-NOV-2000; 2000US-02599P.
17-NOV-2000; 2000US-02599P.
17-NOV-2000; 2000US-025103P.
0S-DEC-2000; 2000US-025198P.
0S-DEC-2000; 2000US-0251868P.
0S-DEC-2000; 2000US-0251868P.
0S-DEC-2000; 2000US-0251868P.
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0S-DEC-2000; 2000US-0251868P.
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Best Local Similarity 100.
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-483426/52.
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2000US-0249214P.
2000US-0249215P.
2000US-0249216P.
2000US-0249218P.
2000US-0249244P.
2000US-0249244P.
2000US-0249264P.
2000US-0249264P.
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2000US-0249299P.
2000US-0249300P.
2000US-0250160P.
2000US-0250391P.
      2000US-0235836P.
2000US-0236367P.
2000US-0236369P.
2000US-0236369P.
2000US-0236369P.
2000US-023630P.
2000US-02370P.
2000US-023703P.
2000US-023703P.
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2000US-023703P.
2000US-023703P.
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2000US-0246475P.
2000US-0246477P.
2000US-0246477P.
2000US-0246478P.
2000US-0246478P.
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20000S-0246526P-
20000S-0246528P-
20000S-024653P-
20000S-0246619P-
20000S-024661P-
20000S-024661P-
20000S-0249208P-
20000S-024921P-
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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13-0CT-2000)
13-0CT-2000)
20-0CT-2000)
20-0CT-2000)
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20-OCT-2000;
01-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
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17-NOV-2(
17-NOV-2(
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
cocivity, and can be used in gene therapy and vaccine production. (I)
corrections and polynuclectides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
consistent the activity of (I) by expressing inactive proteins or to
that affect the activity of (I) by expressing inactive proteins or to
consistent the patients own production of (I). Additionally, (I)
concleic acids into a host cell and culturing the cell to express the
polymucleotides may be used to produce the secreted (I), by inserting the
concleic acids into a host cell and culturing the cell to express the
concern and treat immune/haematopoictic-related diseases, especially
concern and cancer metateases of haematopoictic derived cells. AAK64703
concers and cancer thuman immune/haematopoictic antigen genomic
concerns and the present thuman immune/haematopoictic antigen genomic
concerns and present invention. AAK54942 to AAK54950 and AAM62169
concerns used in the exemplification of the present invention
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                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis
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                                                                                                                                               Disclosure; SEQ ID NO 28503; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21619 BP; 7128 A; 3520 C; 3719 G; 7252 T; 0 U; 0 Other;
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                  Ruben SM
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04-FEB-2000; 2000US-018652BF.
02-MAR-2000; 2000US-0184664F.
16-MAR-2000; 2000US-0189374F.
17-MAR-2000; 2000US-0199076F.
18-ARR-2000; 2000US-0199178F.
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2000US-0215135P.
2000US-0216647P.
2000US-0216880P.
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Best Local Similarity luv..
Best Local Similarity
Local Similarity
Local Similarity
                Rosen CA, Barash SC,
                                                     WPI; 2001-483426/52.
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07-JUL-2000
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AAL07315/c
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14-JUL-2000; 2000US-0218290F-14-JUL-2000; 2000US-0224519F-14-JUC-2000; 2000US-0224519F-14-JUC-2000; 2000US-0224519F-14-JUC-2000; 2000US-0224519F-14-JUC-2000; 2000US-0225266F-14-JUC-2000; 2000US-0225767F-14-JUC-2000; 2000US-0225767F-14-JUC-2000; 2000US-0225767F-14-JUC-2000; 2000US-0225769F-14-JUC-2000; 2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JUC-2000US-0225769F-14-JU
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20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
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The present invention provides the protein and coding sequences of a number of human reproductive system related antiques. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
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94.1%; Score 16; DB 4; Length 21619;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
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20-0CT-2000, 201-00V-2000, 201
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01-DEC-2000;
01-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
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2000US - 0234223 P.
2000US - 0234274 P.
2000US - 0234997 P.
2000US - 023498 P.
2000US - 0235484 P.
                         200005-0231413P.
200005-0231414P.
200005-0232080P.
200005-0232081P.
200005-0231968P.
                                                                  2000US-0232398P.
2000US-0232398P.
2000US-0232400P.
2000US-0232401P.
2000US-0233063P.
2000US-0233064P.
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2000US-0249216P.
2000US-0249217P.
2000US-0249218P.
                                                                                                                    21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
26-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ds.
                                                                                                 Human ovarian and breast cancer associated polymucleotide SEQ ID NO 977
                                                        BP.
                    reregaaceaaraar 5295
                                                                                                                                                                                                                     2000US-0184664P
2000US-0184664P
2000US-0189834P
2000US-0198123P
2000US-0198123P
2000US-021513P
2000US-021513P
2000US-021513P
2000US-021513P
2000US-021513P
2000US-021647P
2000US-021647P
2000US-021680P
2000US-021680P
2000US-021680P
2000US-021680P
2000US-0216819P
2000US-022848P
2000US-022856P
2000US-022856P
2000US-0228513P
2000US-022856P
2000US-0228547P
                                                 1182/c
ABA08182 standard; DNA; 21619
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2000US-0225759P.
2000US-0226279P.
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2000US-0226868P.
2000US-0227182P.
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                                                                                   (first entry)
       TGTGGAAGGAATAAAT
                                                                                                                                                                      WO200155325-A2
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24-FEB-2000;
26-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-AY-2000;
07-JUN-2000;
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30-JUN-2000;
07-JUL-2000;
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26. JUL - 2000)
14. AUG- 2000)
18. AUG- 2000)
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05-SEP-2000;
06-SEP-2000;
                                                                                                                                                         Homo sapiens.
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The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                     Altman P, Prentice J, Phillips J; Johnson F;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Wohlgemuth J, Fry K, Matcuk G, A
Ly N, Woodward R, Quertermous T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene signature HUMGS01315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 361; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TGTGGAAGGAATAATA 17
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                                                                                                                                                                                                                                                 22-OCT-2001; 2001WO-US047856.
                                                                                                                                                                                                                                                                                                 20-OCT-2000; 2000US-0241994P.
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Best Local Similarity 94.1%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        (BIOC-) BIOCARDIA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-636525/68.
                                                                                                                                                   WO200257414-A2
                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUN-1995.
                                                                                                                                                                                                  25-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel genes (ABA07454-ABA08224) and proteins (ABB10743-ABB10980) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, theumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated ovarian and/or breast cancer related nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders, particularly ovarian and/or breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T7; leukocyte; gene expression profiling; allograft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, SEQ ID NO 977; 577pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM;
                                                                                                                                                                        01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-025119P.
                                                                                                                                                                                                                                                                                                                                                   08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251999P.
11-DEC-2000; 2000US-02590PP.
05-JAN-2001; 2001US-0259678P.
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                                                                                                 2000US-0249297P.
2000US-0249299P.
2000US-0249300P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
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                          17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
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ABZ01147;

RESULT 10

Query Match

Matches

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Rosen CA,

PRAKARA BARARA B

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Skokut T,
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                                                                                                                                                                                                                                                                                                                                 A single-stranded DNA (or its complementary strand or the corresp. double stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT1901-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3' -directed DNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly (T) as the sole primer. Since the 3'- untranslated sequence is unique of a particular mRNA peccies, almost all the 3'-end of mRNA by using securately the relative abundance of different mRNAs in the particular issue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell
                                                                                                                                                                                                          Single-stranded DNA for identifying gene signatures - isolated from 3'-directed human cDNA library that reflects relative abundance of corresp. mRNA in specific human tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds; visual phenotype; plant; architecture; leaf surface; chlorotic; bleaching; etching; wet leaf; stunting; elongation; texture; agronomic trait; growth regulation; dwarf variety; insect resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shukla V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 215 BP; 71 A; 32 C; 36 G; 72 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function or for recognising different cell types
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                                                                                                                                                                                                                                                                                             Claim 1; Page 577; 2245pp; Japanese.
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DOW AGROSCIENCES LLC.
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                      93JP-00355504
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nes 16; Conservative
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                                                                                                                           Natsubara K, Okubo K;
                                                              (MATS/) MATSUBARA K.
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                                                                                                                                                                      WPI; 1995-206931/27
                                                                                   OKUBO K.
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                      12-NOV-1993;
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This invention relates to the identification and isolation of novel nucleic acid molecules that confer altered visual phenotypes in plants. Specifically, it refers to modifications of plant architecture and/ or leaf surface features in plants, such as chlorotic, bleaching, etching, wet leaf, stunting, elongation and texture phenotypes, which are thought will be agronomic traits beneficial to the farmer. As such, these novel phenotypes can affect growth regulation i.e. useful for creating dwarf varieties, exhibit resistance to insects or heat stress, confer changes in pigment content such that plants have enhanced vitamin production or delayed senescence and also for example produce plants that control the production of ethylene. Purthermore, the present invention comprises generating transgenic plants, as well as reproducibly altering the visual polynucleotides described herein. This polynucleotide is a homologue of a DNA sequence that confers an altered visual phenotype when expressed in
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Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful for conferring altered visual phenotypes in plants.
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                                                                                                                                                                              Claim 1; SEQ ID NO 1317; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plants, the method of the invention.
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(DOWC ) DOW AGROSCIENCES LLC.
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This invention relates to the identification and isolation of novel nucleic acid molecules that confer altered visual phenotypes in plants. Specifically, it refers to modifications of plant architecture and/ or leaf surface features in plants, such as chlorotic, bleaching, etching, wer leaf, stunting, elongation and texture phenotypes, which are thought will be agronomic traits beneficial to the farmer. As such, these novel phenotypes can affect growth regulation i.e. useful for creating dwarf varieties, exhibit resistance to insects or heat stress, confer changes in pigment content such that plants have enhanced vitamin production or delayed sensescence and also for example produce plants that control the production of ethylene. Furthermore, the present invention comprises contacting transgenic plants as well as reproducibly altering the visual phenotype of plant seeds, plant tissues and plant cells containing the phenotype of plants each, plant tissues and plant cells containing the DNA sequence that confers an altered visual phenotype when expressed in plants, the method of the invention.
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Sequence 601 BP; 178 A; 105 C; 148 G; 170 T; 0 U; 0 Other;

Gaps . 90.6%; Score 15.4; DB 9; Length 601; 94.1%; Pred. No. 6.9e+02; ive 0; Mismatches 1; Indels (Query Match Best Local Similarity 94.15

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RESULT 14

ADD16351 standard; DNA; 602 ADD16351

ADD16351;

BP.

(first entry) 15-JAN-2004 DNA (SeqID 419) that confers an altered visual phenotype in plants.

ds, visual phenotype, plant, architecture, leaf surface, chlorotic, bleaching; etching; wet leaf, stunting, elongation, texture, agronomic trait, growth regulation, dwarf variety; insect resistance, heat stress, transgenic.

WO2003020741-A1.

13-MAR-2003

30-AUG-2002; 2002WO-US027880

31-AUG-2001; 2001US-0316326P.

(DOWC) DOW CHEM CO. (DOWC) DOW AGROSCIENCES LLC.

Shukla V; Ruegger M, Larrinua I, Crosley R, Skokut T, WPI; 2003-300858/29

Oryzae Novel isolated nucleic acid derived from Nicotiana benthamiana, (sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful for conferring altered visual phenotypes in plants.

Claim 1; SEQ ID NO 419; 517pp; English

This invention relates to the identification and isolation of novel nucleic acid molecules that confer altered visual phenotypes in plants. Specifically, it refers to modifications of plant architecture and/ or leaf surface features in plants, such as chlorotic, bleaching, etching, wet leaf, stunting, elongation and texture phenotypes, which are thought will be agronomic traits beneficial to the farmer. As such, these novel phenotypes can affect growth regulation i.e. useful for creating dwarf

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varieties, exhibit resistance to insects or heat stress, confer changes in pigment content such that plants have enhanced vitamin production or delayed senescence and also for example produce plants that control the production of ethylene. Furthermore, the present invention comprises generating transgenic plants, as well as reproducibly altering the visual phenotype of plant seeds, plant tissues and plant cells containing the polymucleotides described herein. This polymucleotide is a homologue of a DNA sequence that confers an altered visual phenotype when expressed in plants, the method of the invention.
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Sequence 602 BP; 182 A; 106 C; 145 G; 169 T; 0 U; 0 Other;

Gaps ö 90.6%; Score 15.4; DB 9; Length 602; 94.1%; Pred. No. 6.9e+02; ive 0; Mismatches 1; Indels 0 16; Conservative Local Similarity Query Match Matches

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ò 셤 RESULT 15 AAH31558

ВЪ AAH31558 standard; cDNA; 657

AAH31558;

(first entry) 30-JUL-2001 Human olfactory receptor polynucleotide, SEQ ID NO: 131

Human, olfactory receptor, OR, primary scent determination, secondary scent determination, polypeptide library, odour receptor; scent profile; scent fingerprint; scent representation; ss.

Homo sapiens.

WO200127158-A2

19-APR-2001

06-OCT-2000; 2000WO-US027582.

99US-0158615P. 24-FEB-2000; 2000US-0184809P 08-OCT-1999;

(DIGI-) DIGISCENTS. (YEDA) YEDA RES & DEV CO LTD.

Fuchs T, Lancet D, Glusman G, Bellenson J, Smith D,

WPI; 2001-290713/30.

New polynuclectides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.

Claim 1; Fig 2; 1857pp; English.

The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the doour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals

Sequence 657 BP; 171 A; 124 C; 160 G; 165 T; 0 U; 37 Other;

Query Match

90.6%; Score 15.4; DB 4; Length 657;

Best Local Similarity 94.1%; Pred. No. 6.9e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps

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Search completed: March 25, 2004, 10:25:16 Job time : 21.642 secs

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BU898228 X076G05 P
BU898227 X076G05 P
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1. (bases 1 to 362)

1. (bases 1 to 362)

1. Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, M., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.

Insight into hepatocallular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15099-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
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AQ265092
CE748440
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BG838806
BM08325174
BG651500
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                                                                     March 25, 2004, 09:53:09; search time 128.47 Seconds (without alignments) 3951.570 Million cell updates/sec
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          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                    27513289 seqs, 14931090276 residues
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Maximum Match 100%
Listing first 45 summaries
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Searched:

Sequence:

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Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Other GSS: CIT-HSP-2382B13.TR
Contact: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13.21
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 510)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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HS 2063 A2 G01 MR CIT Approved Human Genomic Sperm Library D Homo
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AQO80438 445 bp DNA linear GSS 20-AUG-1998 CIT-HSP-2382B13.TF CIT-HSP Homo sapiens genomic clone 2382B13, genomic survey sequence.
                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. (base); Lo 48, S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Sperm"
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KhoI:
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    Fax: 86-21-50801922
Email: hazzgedigc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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I (bases 1 to 652)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Simon, M. and Venter, J.C.
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
Unpublished (1998)
Other GSSs: CIT-HSP-2342D16.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ055707 652 bp DNA linear GSS 30-JUL-1998
CIT-HSP-2342D16.TR CIT-HSP Homo Rapiens genomic clone 2342D16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                              /sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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100.0%; Score 17; DB 28; Length 510;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 17; Conservative 0; Mismatches 0; Indels
              Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Faz: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2063 row: M column: 2
                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/clone="Plate=2063 Col=2 Row=M"
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                                                                                                                                                                                                           High quality sequence stop: 510.
Location/Qualifiers
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AQ055707.1 GI:3352313
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Homo sapiens
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AQ055707
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BJ572614 Ipomoea nil mixture of flower and flower bud Ipomoea nil cDNA clone jm21e10 3', mRNA sequence.
BJ572614 IG:27254442
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BJ571448 I GI:27253276
EST.
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(Dases 1 to 684)
Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,T., Nitaeaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S. Unpublished (2002)
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/db_xref="imilelo"
/clone="jmilelo"
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/clone_lib="Ipomoea nil mixture of flower and flower bud"
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Incomes and
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Convolvulaceae; Ipomoea.
1 (bases 1 to 773)
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/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
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                                                                                                                                                                                                   Indels
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Wishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                                                                           100.0%; Score 17; DB 28;
100.0%; Pred. No. 2.2e+03;
vative 0; Mismatches 0;
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Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyea; eudicoryledons; core eudicots; asterios; lamiids; Solanales; Convolvulaceae; Ipomoea.

1 (Dases 1 to 791)

1 (Dases 1 to 791)

2 Hoshino, A., Seki, M., Shin i, T., Carninci, P., Kamiya, A., Shiraki, T., Nitaesaka, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S. ESTS of Japanese morning glory

1 Unpublished (2002)

1 Contact: Tadasu Shin, C.

1 Center For Genetic Resource Information

National Institute of Genetics

11 Yata, Mishina, Shizucka 411-8540, Japan

Tel: 81-559-81-6855
                                                                            BJ567603 Ipomoea nil mixture of flower and flower bud Ipomoea nil BJ567603 BJ567603 GI:27249423 EST.
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BJ570146 GI:27251974
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[ (Dases 1 to 814)
Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T., Nitaaaka, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S. ESTs of Japanese morning glory
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mkNa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 17; DB 12; Length 791; larity 100.0%; Pred. No. 2.1e+03; Conservative 0; Mismatches 0; Indels C
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6856
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Location/Qualifiers
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         72 TGTGGAAGGAATAAATA 56
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Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T., Nitaska, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S. ESTS of Japanese morning glory
Unpublished (2002)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Inter For Genetic Resource Information
National Institute of Genetics
Ill1 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
Fax: 81-559-81-6856
Fax: 1-559-81-6856
Fax: 1-6052
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(bases 1 to 781)
Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T., Miaaska, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S. Uppublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6856
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100.0%; Score 17; DB 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                          /organism="Ipomoea nil"
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Location/Qualifiers
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Matches 17; Conservative
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       AUTHORS
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Gaps

Email: tshini@genes.nig.ac.jp.

FEATURES

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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1179)
II, W B., Gruber. C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:12790406.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 ENPX cedex - France
BM 219 191006 ENPX cedex - France
Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
Library was constructed com Contact in Feng Liang Email: Grand@lifetech.com URL:
Location/Qualifiers
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AL526913
                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyra; endicotyledons; core eudicots; asterids; lamiide; Solanales; Convolvulaceae; Ipomoea.

(bases 1 to 831)
Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,T., Nitaeaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S.
Unpublished (2002)
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                                                                                                                                                                                                                                                           Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Tals 11 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
  Ipomoea nil (Japanese morning glory)
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( Dases 1 to 815)

Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,T., Nitasaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S.
Unpublished (2002)
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                                                                         /mol_type="mkNa"
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/mol_type=_mRNA;
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/db_xref="taxon:35883"
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/clone_lib="Ipomoea nil mixture of flower and flower bud"
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Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels C
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Miehima, Shizuoka 411-8540, Japan
Feb: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [pomoea nil (Japanese morning glory)
                                                     organism="Ipomoea nil"
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17; Conservative 0;
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S Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
Carninch, P., Endo, T., Fukuda, S., Akiyama, J., Farakawa, T.,
Carninch, P., Endo, T., Fukuda, S., Enjikawa, J., Ishikawa, T., Itoh, M.,
Hirozane, T., Hori, F., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadgawa, H., Kal, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,
Kusakabe, M., Matsuvama, T., Miki, R., Mizuno, Y., Nakamura, N.,
Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,
Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,
Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A.,
Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,
Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-resigne.riken.go.jp,
URL.ihttp://genome-gescriken.go.jp,
URL.ihttp://genome-gescriken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Saski,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Saski,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y., Ozawa,Y., Muramatsu,M.,
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Yoshhide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                             Length 1179;
                                                                          95.3%; Score 16.2; DB 9; Length 1 ilarity 88.2%; Pred. No. 4.6e+03; Conservative 2; Mismatches 0; Indels
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Email: genome-res@gec.riken.go.jp,
URL:http://genome.gec.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Carninci,P., Okazaki,Y., Wintamatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length trehalose and its application for the synthesis of full length IcDNA, Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1el: 81-45-503-9222
/clone lib="RIKEN full-length enriched, 6 days neonate medulla oblongata"
/note="Site_1: Site_2: BamH; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was GAGAGAGAGAGCACCAAGAGCTTTTTTTTTTTTVN 3'], cDNA was
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 TGTGGAAGGAATAAAT 114
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us-09-963-285-1_copy_359_375.rst

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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
Contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5. Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research bin Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [6. Genome Experiment Contributed to Contributed to Contributed to Contributed to Contributed to Contribute and subsequently enriched for full-length by
cap-trapper. cDNA was prepared with the primer adapter of
strand cDNA was prepared with the primer adapter of
strand cDNA was prepared with the primer adapter of
strand cDNA was cleaved with Xhol and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."
Tomaru,Y., Carminci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carminci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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1. .224
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SOURCE
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Query Match

94.1%; Score 16; DB 10; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels

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Gaps , 0

Search completed: March 25, 2004, 15:30:09 Job time : 133.47 secs

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APPLICANT: Buechler, Joe
APPLICANT: Buechler, Joe
APPLICANT: Walkirs, Gunars
APPLICANT: Gray, Jule
APPLICANT: Lonberg, Mils
TILLE REFERENCE: 020015-000200US
CURRENT APPLICANT: NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-456-090A-99
Sequence 99, Application US/09456090A
, Patent No. 6680209
                                                                                                                                                                                                                                                                                                                                                              6566132 US/09843376
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Best Local Similarity 94.1
Matches 16; Conservative
             2190
2190
2518
2739
3252
3468
3742
5173
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6320
6574
8351
8351
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ORGANISM: Homo sapiens
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: (1)..(675)
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US-09-843-376-10
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NAME/KEY: (
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                US-09-843
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Sequence 26, Appli
Sequence 7, Appli
Sequence 335, bro
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Sequence 1, Appli
Sequence 1175, A
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 16, Appli
Sequence 17, Appl
Sequence 17, Appl
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Sequence 53, Appl
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Appl
Sequence 99, Appl
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                                                                                  March 25, 2004, 09:55:14; Search time 3.34382 Seconds (without alignments) 2821.370 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-621-976-11175

US-09-810-651-1

US-08-813-591-1

US-09-398-4128-1

US-09-734-675-3

US-09-128-155-17

US-09-495-050A-121

US-08-365-171E-53

US-08-365-171E-53

US-08-965-171E-53
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US-09-568-816A-7
US-09-328-111-335
US-09-091-590A-4
US-09-328-111-533
US-08-998-416-353
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                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                   682709 segs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                            US-09-963-285-1_COPY_359_375
17
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Maximum Match 100%
Listing first 45 summaries
                                                            nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seg length: 200000000
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Match Length
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84.7 176373
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1127
16592
36741
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No.
                                                                                          Run on:
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APPLICANT: C. Frank Behnert
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANITENSE MODULATION OF INTERFERON GAMMA RECEPTOR 1 EXPRESSION
FILE REFERENCE: RTS-0234
CURRENT APPLICATION NUMBER: US/09/843,376
CURRENT FILING DATE: 2001-04-26
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 10
LENGTH: 26000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Sequence 1028, Ap Sequence 1, Appli Sequence 29, Appl Sequence 10, Appli Sequence 10, Appli Sequence 2, Appli Sequence 1370, Ap Sequence 1370, Appli Sequence 260, Appli Sequence 1370, Appli Sequence 1370, Appli Sequence 1370, Appli Sequence 1370, Appli Sequence 1370, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135, Appli Sequence 135
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Sequence 3
Sequence 1
Sequence 1
Sequence 1
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                                                                                         US-08-887-5348-29
US-09-527-431-29
US-09-743-871B-10
US-08-951-871-1
US-08-751-871-1
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US-08-956-171E-85
US-08-961-527-139
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Pred. No. 95;
0; Mismatches
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Gaps
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                                                                                                                  COUNTRY: .....
ZIP: 77027
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/169,119
FLING DATE: 09-OCC-1998
CLASSIFICATION: *Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1713-850-0165
JINFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARCTERISTICS:
LENGTH: 313 base pairs
TYPE: INCleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1...313
OTHER INFORMATION: /standard_name= "Rabbit CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11175, Application US/09621976

Patent No. 6639063

GRNERAL INPORMATION:
APPLICANT: Underty, S. APPLICANT: JODert, S. APPLICANT: Glockano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 11175

LENGTH: 391
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STRIE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence S1-1"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 TGTGGAAGGAAGAAT 175
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Best Local Similarity 93.8
Matches 15; Conservative
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Matches 15; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-621-976-11175
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; GENERAL INFORMATION:
; APPLICANT: Dunbar, Bonita S.
TITLE OF INVENTION: Method of Preparation and Use for Zona
TITLE OF INVENTION: Pellucida Antigens and Antibodies for Sterilization and Contraception
                                                                                                                                                                                                                                                                                                                                                                                                Method of Preparation and Use for Zona
Pellucida Antigens and Antibodies for Sterilization and
Contraception
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                                                               DB 4; Length 675; 96;
                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,452
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Pravel, Hewitt, Kimball & Krieger
1177 West Loop South, 10th Floor
                                                                 Score 15; DB 4; Pred. No. 96; 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 30-ARE-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger. Denise M.
TELEPHONE: 713-850-0999
TELEPHONE: 713-850-0909
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1177 West Loop South, 10th
CITY: Houston
STATE: Texas
COUNTY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            RESULT 3
US-08-396-452-1/C
US-08-396-452-1/C
Sequence 1, Application US/08396452;
Sequence 1, Se20663;
GENERAL INFORMATION:
APPLICANT: Dunbar, Bonita S.
TITLE OF INVENTION: Pellucida Anti-
TITLE OF INVENTION: Contraception;
TITLE OF INVENTION: Contraception;
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimba
                                                                 Query Match
Best Local Similarity 100.0%; P:
Matches 15; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 TCTCGAAGAAATAAAT 83
                                                                                                                                                                                             162 TGGAAGGAATAATA 176
                                                                                                                                                        3 TGGAAGGAATAATA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 313 base pairs
nucleic acid
3DNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
  ; OTHER INFORMATION: M2-20H
US-09-456-090A-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: CDNA
US-08-396-452-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 15;
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US-09-169-119-1/c
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TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
MOLECULE TYPE: CDNA tO MRNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-813-591-1
                             JS-08-813-591-1
                                                                  Sequence 1, Application US/09500651
GENERAL INFORMATION:
APPLICANT: ASANO, MINAO
APPLICANT: KAMAI, MISAKO
APPLICANT: MINA, TETSUYA
APPLICANT: MINA, TETSUYA
APPLICANT: MINO, MORIKI
TITLE OF INVENTION: HYDROLYSING A PROTEIN WITH THE SAME
TITLE OF INVENTION: HYDROLYSING A PROTEIN WITH THE SAME
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITT: AALINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

84.7%; Score 14.4; DB 1; Length 1056;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1.9—
OTHER INFORMATION: /note= "INSERTION SEQUENCE, METHOD CHER INFORMATION: OF DETERMINING THE CHARACTERISTICS: B"
US-09-500-651-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "METHOD OF DETERMINING THE CHARACTERISTICS: P"
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION WINBER:
FILING DATE: 14-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORWAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-845-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                      ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIPTICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/813,591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
MOLECULE TYPE: CDNA tO MRNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEGURACE CHARACTERISTICS:
LENGTH: 1056 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 1..1056
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                          COUNTRY:
                                                       US-09-500-651-1
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Gaps
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                                                                                                                                                        /note= "INSERTION SEQUENCE, METHOD OF DETERMINING THE CHARACTERISTICS: E"
                                      /note= "METHOD OF DETERMINING THE CHARACTERISTICS: P"
                                                                                                                                                                                                                                                                                                                                        2 GTGGAAGGAATAAATA 17
                                                                                                               NAME/KEY: misc_feature
NAME/KEY: CDS
LOCATION: 1..1056
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                  LOCATION: 1..9 OTHER INFORMATION:
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RESULT

436 GTAGAAGGAATAATA 451

Gaps ö

436 GTAGAAGGAATAATA 451

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RESULT 12
US-09-495-050A-121
US-09-495-050A
Sequence 121, Application US/09495050A
Patent No. 6492505
GENERAL INFORMATION:
APPLICANT: Roopa, Reddy
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED FILE REPERENCE: PA-013 US
CURRENT APPLICATION NUMBER: US/09/495,050A
CURRENT FILING DATE: 2000-01-31
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Sequence 17, Application US/09128155

Patent No. 6117654

GENERAL INFORMATION:

APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

TITLE OF INVENTION: AND USES THEREOF

TILLE PREPRENCE: 09404/052001

CURRENT FILING DATE: 1999-08-03

FARLIER APPLICATION NUMBER: US/09/126,155

CURRENT FILING DATE: 1998-07-02

FARLIER PLICATION NUMBER: US 60/091,650

FARLIER PLILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PastSEQ for Windows Version 3:0

SEQ ID NO 17

LENGTH: 176373
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.7%; Score 14.4; DB 3; Length 176373; 93.8%; Pred. No. 3.68+02; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                          Query Match

84.7%; Score 14.4; DB 3; Length 152331;
Best Local Similarity 93.8%; Pred, No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0;
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILLING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FaetSEQ for Windows Version 3.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (1)...(176373)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                               FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(152331)

OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                        LENGTH: 152331
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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US-09-128-155-17
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                                                                         GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-lzeta, related reage TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-lzeta, related reage TITLE OF INVENTION: Mathods
FILE REFERENCE: DX0904K
CURRENT APPLICATION NUMBER: US/09/398,4128
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: US 60/100948
PRIOR FILING DATE: 1998-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOOGRES
CURRENT APPLICATION NUMBER: US/09/734,675
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 38844
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US-09-128-155-16/C
| Sequence 16, Application US/09128155 |
| Patent No. 611/654 |
| GENERAL INFORMATION: |
| APPLICANT: Pan, Yang |
| TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY |
| TITLE OF INVENTION: AND USES THEREOF |
| FILE REPREMENCE: 09404/052001 |
| CURRENT APPLICATION NUMBER: US/09/128,155 |
| CURRENT PILING DATE: 1998-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.7%; Score 14.4; DB 4; Length 1225; 93.8%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                            ; Sequence 1, Application US/09398412B
; Patent No. 6680380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09734675
Patent No. 6365391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30049 reresaacearaaar 30064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGTGGAAGGAATAAAT 16
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TGTGGAAGGAATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: CDS
; LOCATION: (491)..(1144)
; OTHER INFORMATION:
US-09-398-4128-1
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
       US-09-398-412B-1/c
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156 TGTGGAAGGAATAA 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08392546C

Sequence 4, Application US/08392546C

Patent No. 5874298

GENERAL INFORMATION:
APPLICANT: Johnson, Janice, Kral, Robert M. Jr., Krapcho, Karei, TILE OF INVENTION:
INDRER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MADSON & METCALF
STREET: 950 FIRST INTERSTATE BUILDING
STREET: 170 SOUTH MAIN STREET
CITY: SALT LAKE CITY
STATE: UTAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1127,
                                                                                                                                                                                                                                                                                                                    Ouery Match 82.4%; Score 14; DB 4; Length 234; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
PRIOR APPLICATION NUMBER: 60/118,318

PRIOR FILING DATE: February 1, 1999

NUMBER OF SEQ ID NOS: 305

SOCTWARE: PERL Program

SEQ ID NO 121

LENGTH: 234

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

NAME/KEY: misc_feature

JUNGE/KEY: misc_feature

US-09-495-050A-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 84101
COMPUTER READABLE FORM:
MEDIUM TYPE Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.4%; Score 14; DB 2; Le Best Local Similarity 100.0%; Pred. No. 3.2e+02; Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bracon hebetor
INDIVIDUAL ISOLAIE: 30 kDa toxin cDNA
05-08-392-546C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,546C
FILLING DATE: 2/17/95
ATTORNEY AGENT INFORMATION:
NAME: L. CRAIG METCALF
REGISTRATION NUMBER: 31,398
REFERENCE/DOCKET NUMBER: 1094.2.3
TELECOMMUNICATION INFORMATION:
TELEFHONE: (801) 537-1799
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1127 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                        3 TGGAAGGAATAAAT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown MOLECULE TYPE: cDNA HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-392-546C-4
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PRESIDE.

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; FILE REFERENCE: UT$H:243
; CURRENT APPLICATION NUMBER: US/09/301,665
; CURRENT APPLICATION NUMBER: 60/083,408
; EARLIER APPLICATION NUMBER: 60/083,408
; EARLIER PILING DATE: 1998-04-29
; EARLIER FILING DATE: 1998-04-29
; EARLIER FILING DATE: 1998-04-28
; NUMBER OF SEQ ID NOS: 4
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 36/41
; TYPE: DAM 3
; ORGANISM: Homo sapiens
US-09-301-665-3

Query Match
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels

QV
3 TGGAAGGAATAAAT 16

DD 35/48 TGGAAGGAATAAAT 35735
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0; Gaps

Search completed: March 25, 2004, 15:34:21 Job time: 4.34382 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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Transcription factor; FOXC2; antidiabetic; anorectic; antilipaemic; cardiovascular; FOXC2 promoter; cardiovascular; FOXC2 promoter; diabetes mellitus; obesity; hypercholesterolaemia; dyslipidaemia; cardiovascular disease; mouse medenchyme forkhead 1; MHF-1; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated FOXC2 promoter region that modulates the expression of a FOXC2 polypeptide is useful for treating obesity and type II diabetes mellitus.
                                                                                         Genomic DNA encoding mouse mesenchyme forkhead-1 (MHF-1)/FOXC2
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^+tag= a
/product= "MHF-1 or FOXC2"
/note= "Mouse mesenchyme forkhead
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                      BP
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10-OCT-2000; 2000US-0238897P.
09-NOV-2000; 2000SE-00004102.
                       ABK48986 standard; DNA; 6021
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                                                                     (first entry)
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P-PSDB; AAU79818.
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                                              ABK48986;
RESULT 1
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/note= "Region coding for 5'part of alternative protein"
The invention describes an isolated human FOXC2 promoter region. The mammalian FOXC2 promoter region for the medulation of FOXC2 polypeptide expression has therapeutic value in treating type II diabetes mellitus, obsity, hypercholesterolaemia, other cardiovascular diseases or dyslipidaemias. This sequence encodes the mouse mesenchyme forkhead if (MHF-1) protein (also called FOXC2 transcription factor), described in the method of the invention
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= e //rtag= of the FOXC2 enhancer. Specifically claimed in claim 16"
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hote= "Fragment of the FOXC2 promoter. Specifically
claimed in claim 3"
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/note= "First exon according to the alternative
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1. .186
                                                                                                                                                 Sequence 6021 BP; 1350 A; 1675 C; 1642 G; 1354 T; 0 U; 0 Other;
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                                                                                                                                                                                    100.0%; Score 25; DB 6; Length 6021; larity 100.0%; Pred. No. 0.79; Conservative 0; Mismatches 0; Indels
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note= "Alternative first exon splice site"
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/note= "Fragment of the FOXC2
claimed in claim 12"
359. .375
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/note= "Fragment of the FOXC2
claimed in claim 13"
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note= "Portion of polypeptide used in alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6458 BP; 1443 A; 1826 C; 1715 G; 1474 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                               *tag= p
'note= "Region coding for DNA-binding domain"
!516. .4629
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100.0%; Pred. No. 0.79;
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/*tag= j
clote= "Fragment of the FOXC2 promoter.
claimed in claim 2"
1692. 1703
/*tag= "Fragment of the FOXC2 promoter.
claimed in claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
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note= "Second exon according
                                                                                                                                                                                                                                                                                                                                             note= "Transcription factor"
448. .2735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rondahl L,
                                                                                                                                                                                                                                                                                                            *tag= o
product= "FOXC2"
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10-OCT-2000; 2000US-0238897P.
09-NOV-2000; 2000SE-00004102.
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25; Conservative (
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2516. .3740
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3741. .4629
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235. .3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An isolated FOXC2
FOXC2 polypeptide
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ADA72007;

RESULT 3 ADA72007 gene; ds.

Plant;

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The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also cincluded is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (BST) for inforensics, in assessing biodiversities, or in identifying mutations in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, or chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence is useful for part of the printed specification, but was for this patent did not form part of the printed specification, but was obtained in electronic formet directly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide sequences obtained from various cDNA libraries, useful
                                                                                                                                                                                                                                                               ss; sequencing by hybridisation; SBH; expressed sequence tag; mapping; biodiversity; genetic disorder.
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or in generating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18.8; DB 8; Length 4
Pred. No. 2.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as hybridization probes, as oligomers for PCR, for mapping, in the recombinant production of protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seqdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 26403; 44pp; English
                              13970 ATTCCACAAATATACAAACTATCC 13993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stache-Crain B,
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 TACACAAAAAAACAACTGTCC 397
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                                                                                                                      ВР.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               0-JUL-2001; 2001US-00918995
                                                                                                                    ACH39191 standard; cDNA; 455
                                                                                                                                                                                                                              Human foetal brain cDNA #558
                                                                                                                                                                                            13-OCT-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LABAT I.
STACHE-CRAIN E
DICKSON M C.
JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antisense DNA or RNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRMANAC R T.
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                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                          ACH39191;
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STAC/)
DICK/)
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                                                                                                                                                                                                                                                                  Human;
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                                                                                     RESULT 5
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1 LOCUS ABQ84281 Accession Abg84281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant
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                                                                                                                                                            bacterial infection; fungal infection; viral infection; rice;
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T, Zou
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Whitham S, Xie Z,
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Pred. No. 2.5e+02;
); Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID NO 5332; 899pp; English.
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410000
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fragments
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S, Tao Y,
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nilarity 87.5%;
Conservative
                 ADA72007 standard; DNA; 1019
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200001
300001
400001
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                                                                                     (first entry)
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es 21; Conservative
                                                                                                                       Rice gene, SEQ ID 5332
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it into 5
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ABQ84281 0
ABQ84281 1
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ABQ84281 3
ABQ84281 3
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ABOGA281.1
Continuation (2 of
WP Sequence split i
WP Fragment Nam
WP ABOGA281.0
WP ABOGA281.1
WP ABOGA281.2
WP ABOGA281.2
WP ABOGA281.3
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Katagiri F,
                                                                                     20-NOV-2003
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Gaps

Query Match Best Local S

Matches

Query Match

Matches

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RESULT 6 ACH40492

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Human, transmembrane protein, 65h2 protein, 593 protein, prostaglandin,
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                                                                                                                                         Nucleotide sequence of a human transmembrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 181-194; 215pp; English.
                                                                                                                                                                                                              thromboxane, KIAA0880 protein; ss
AAF54867 standard; DNA; 50000 BP
                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000; 2000WO-US020521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-1999; 99US-00365162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC.
                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-138648/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predictive medicine.
                                                                                                                                                                                                                                                                                                          WO200109185-A2.
                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                         15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Curtis RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF54868;
                                             AAF54867;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50811, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The mucleic acid sequences are reading frame of the novel polynucleotide. The mucleic acid sequences of the novel polynucleotide. The mucleic acid sequences in forensics, in assessing biodiversities, or in identifying mutations in forensics, in assessing biodiversities, or in identifying mutations in forensics, and gene mapping, in the recombinant production of corticomes are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of corticomes are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of so useful for generating antisense DNA or RNA. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data corticom that production of cortained in electronic format directly from USPTO at sequence cortained in electronic format directly from USPTO at sequence cortained in electronic format directly from USPTO at sequence cortained sequence.
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                                                                                                                                                                                                                                                                                         Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 464 BP; 135 A; 98 C; 109 G; 116 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 27704; 44pp; English.
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                                                                                                 ACH40492 standard; cDNA; 464 BP.
                                                                                                                                                                                                                                        Human foetal brain cDNA #1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUL-2001; 2001US-00918995.
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                                                                                                                                                                                          (first entry)
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LABAT I.
STACHE-CRAIN B.
DICKSON M C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Labat I,
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                                                                                                                                                                                                                                                                                                                                                                                                            JS2003073623-A1
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                             13-OCT-2003
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(LABA/) I
(STAC/) S
(DICK/) I
(JONE/)
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The present sequence encodes a human transmembrane protein. The specification describes transmembrane proteins designated KIAA0880, 65h2 and 591. The proteins and polymuclochides can be used for screening assays, detection assays, e.g. chromosome mapping, tissue typing, forensic blology and predictive medicine, e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics. They polymucleoties an also be used for the recombinant production of 65h2 and 533 proteins, which can be used in assays to detect compounds which modulate their activity. These compounds are useful in the treatment of diseases characterized by aberrant activity or expression of protein which catalyse or facilitate transport of charged organic compound, e.g. prostaglandins and thromboxanes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, transmembrane protein, 65h2 protein, 593 protein, prostaglandin, thromboxane, KIAA0880 protein, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 50000 BP; 13944 A; 11451 C; 11177 G; 13428 T; 0 U; 0 Other;
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75.2%; Score 18.8; DB 4; Length 50000;
Best Local Similarity 90.9%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic nucleotide sequence of a human 65h2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1142 Tacacaaaaaaacaaacrercc 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 TCCACAAATAAACAAACIGIC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF54868 standard; DNA; 81145 BP
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RESULT 7 AAF54867/C

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The present sequence encodes a human transmembrane proteins designated 65h2. The specification also describes a transmembrane protein designated 593 and KIAA0880. The proteins and polynucleotides can be used for screening assays, detection assays, e.g. chromosome mapping, tissue typing, forensic biology and predictive medicine, e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomies. They polynucleotides can also be used for the recombinant production of 65h2 and 593 proteins, which can be used in assays to detect compounds which diseases characterized by aberrant activity or expression of protein which catalyse or facilitate transport of charged organic compound, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice endosperm expression sequence label and genechip prepared from it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice; endosperm expression sequence label; gene chip; babel technique;
                                                                                                                                                                                              New nucleic acid molecules encoding transmembrane proteins designated 65h2 and 293 are useful for screening assays, detection assays and in predictive medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 81145 BP; 22396 A; 18624 C; 18484 G; 21641 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.2%; Score 18.8; DB 4; Length 81145; 90.9%; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice endosperm expression sequence label #23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                            Disclosure, Fig 1L1-1L36, 215pp, English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostaglandins and thromboxanes
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                                             28-JUL-2000; 2000WO-US020521
                                                                           99US-00365162
                                                                                                        (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 90.9
Matches 20; Conservative
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                                                                                                                                                                   WPI; 2001-138648/14.
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                                                                           30-JUL-1999;
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                08-FEB-2001
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                                                                                                                                       Curtis
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                                          The invention describes a novel rice endosperm expression sequence label and the gene chip formed from it. The expression sequence babel technique is used to create a rice endosperm cDNA library. Non-redundant expression sequence labels are then combined and used to create a gene chip by microarray techniques. This sequence represents a rice endosperm expression sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the 613 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter specially inked to the mucleic acid mucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide whose expression is inhibited by the mutisense mucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Xu HH;
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                                                                                                                                                                                                           74.4%; Score 18.6; DB 7; Length 494; 84.0%; Pred. No. 2.9e+02; tive 0; Mismatches 4; Indels (
                                                                                                                                                                            Sequence 494 BP; 132 A; 117 C; 102 G; 143 T; 0 U; 0 Other;
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Forsyth RA,
                   Claim 1; Page 18 (Disclosure); 29pp; Chinese.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; SEQ ID NO 22176; 1766pp; English.
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Carr GJ,
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06-SEP-2001, 2001US-00948993.
25-OCT-2001, 2001US-0342923P.
08-FEB-2002, 2002US-00072851.
06-MAR-2002, 2002US-0362699P.
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                                                                                                                                                                                                                                                   21; Conservative
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-029926/02
                                                                                                                                                                                                                                Best Local Similarity
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ACA34306/
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the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation; (8) athway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts, (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or which each of the strains is present in a culture or collection of product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the correling or organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target or prolatering discovery price assential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genomic polynucleotide SEQ ID NO 18493.
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Pred. No. 3.7e+02;
0; Mismatches 1; Indels (
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Best Local Similarity 95.0
Matches 19; Conservative
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Continuation (10 of 19) of AAT42063 from base 900001 (Haemophilus influenzae complete gf
WP Sequence split into 19 fragments LOCUS AAT42063 Accession Aat42063
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discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB77202). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 5.4e+02;
); Mismatches 1;
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95.0%;
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                                                                                                                                                                                                            Query Match
Best Local Similarity 95.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid array containing Xenopus embryonic nucleic acids is useful to identify genes involved in embryonic development, to identify different types of embryonic cells, and to diagnose developmental
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Frog, ss; embryonic development; developmental disorder; microarray; cell differentiation.
                                                     Length 110000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.8%; Score 18.2; DB 6; Length 686; larity 87.0%; Pred. No. 4.4e+02; Conservative 0; Mismatches 3; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 686 BP; 187 A; 144 C; 170 G; 184 T; 0 U; 1 Other;
                                                                                          1; Indels
                                                  Score 18.4; DB 2;
Pred. No. 5.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                Frog embryonic gene sequence Q9925471.
1810000
                                                                                                                                                            5260 CCACAATAACAACTTTC 5279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 348; 823pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Altmann CR;
                                                                                                                             5 CCACAAATAAACAAACTGTC 24
                                                                                                                                                                                                                                                      ABS77078 standard; cDNA; 686 BP
                                                    73.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUL-2001; 2001US-00910943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-2000; 2000US-0219658P.
1700001
                                        Query Match
Best Local Similarity 95.0%
....has 19; Conservative
                                                                                                                                                                                                                                                                                                                           12-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hemmati-Brivanlou A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2002081610-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kenopus laevis.
AAT42063_17
AAT42063_18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders
                                                                                                                                                                                                                                                                                         ABS77078;
                                                                                                                                                                                                                   RESULT 14
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0; Gaps

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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30694.
                                                                                            Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
         345 CAGTCCACAATGACCAAACGGT 323
1 CAGTCCACAATAAACAAACTGT 23
                                            BP
                                                                                                                                                                                                                                                                2000US-0218290P.
2000US-0220963P.
2000US-0220964P.
                                                                                                                                                                                                                                                                                                                          000US-0225268P.
                                                                                                                                                       17-JAN-2001; 2001WO-US001354.
                                                                                                                                                                                                                                                                                                       000US-0225214P
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0231243P
                                            AAK75882 standard; DNA; 5124
                                                                    07-NOV-2001 (first entry)
                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                              26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                .9-MAY-2000;
                                                                                                                                                                                                                      07-JUN-2000;
                                                                                                                                                                                                                                   0-JUN-2000;
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                                                                                                                                                                                                                                                                                                                          4-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                             2-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-2000
                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                    4-AUG-2000
                                                        AAK75882;
                               RESULT 15
                                      AAK75882
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2000US-0246475P.
2000US-0246476P.
2000US-0246477P.
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17-NOV-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
cativity, and can be used in gene therapy and vaccine production. (I)
cytoteins and polynuclectides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
cypression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
cyplument the patients own production of (I). Additionally, (I)
cypolynucleotides may be used to produce the secreted (I), by inserting the
nucleic acids into a host call and culturing the call to express the
cyctein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic derived cells. AAK64703
concerns and cancer human immune/haematopoietic antigen genomic
sequences from the present invention. AAK84992 to AAK84950 and AAM82169
crepresent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 30694; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5124 BP; 1322 A; 1253 C; 1083 G; 1466 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
72.8%; Score 18.2; DB 4; Length 5124;
Best Local Similarity 87.0%; Pred. No. 5.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA, Barash SC, Ruben SM
                              2000US-0249399
2000US-02493009
2000US-02503160
2000US-02510309
2000US-02510309
2000US-02510309
2000US-02514989
2000US-02514989
2000US-02518689
2000US-02518689
                                                                                                                                                                                                                                                            2000US-0251989P
2000US-0251990P
                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-483426/52.
                                                    17-NOV-2000;
01-DBC-2000;
05-DBC-2000;
05-DBC-2000;
05-DBC-2000;
06-DBC-2000;
08-DBC-2000;
08-DBC-2000;
08-DBC-2000;
08-DBC-2000;
08-DBC-2000;
08-DBC-2000;
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Gaps

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Search completed: March 25, 2004, 10:25:20 Job time : 29.9441 secs

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Sequence 1, Appli
Sequence 24, Appl
Sequence 24, Appl
Sequence 1426, Ap
Sequence 2355, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 11, Appli
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Sequence 24, Appli
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Sequence 1103, Appli
Sequence 1103, Appli
Sequence 1103, Appli
Sequence 1103, Appli
Sequence 1103, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 1830121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:

CORRESCONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE PORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: POLI Pentium
OPERATING SYSTEM: MS DOS v6.22
COMPUTER: AD11 Pentium
OPERATING SYSTEM: MS DOS v6.22
COMPUTER: AD11 Pentium
OPERATING SYSTEM: MS DOS v6.22
COMPUTER: AD21 Pentium
OPERATING SYSTEM: MS DOS v6.22
COMPUTER: AD41 Pentium
OPERATING SYSTEM: MS DOS v6.22
CURRENT APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
FILING DATE: 1NN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: MACHOLIS & MATKS
REGISTRATION NUMBER: 41,91
REFERENCE/DOCKET NUMBER: P9186P3
TELEPAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
CURRENT DATE CAID
                    US-09-319-056B-22
US-09-319-056B-24
US-09-107-532A-2355
US-09-223-134-1
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US-09-223-134-1
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US-09-134-465-11
US-09-134-465-11
US-09-134-000C-2101
US-09-134-000C-2101
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US-09-134-000C-2101
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Best Local Similarity 95.0%; Pred. No. 76;
Matches 19; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
US-09-557-884-1
'Sequence 1, Application US/09557884
'Setent No. 6506581
'CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 CCACAAATAAACAAACTGTC 24
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                                                                                            Sequence 1, Applisequence 19, Applisequence 195, Applisequence 2650, Applisequence 3, Applisequence 3, Applisequence 17, Applisequence 17, Applisequence 17, Applisequence 17, Applisequence 1109, Applisequence 1109, Applisequence 2595, Applisequence 5, Applisequence 5, Applisequence 5, Applisequence 5, Applisequence 5, Applisequence 5, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequ
                                                                                                                                              March 25, 2004, 09:55:14 ; Search time 4.91739 Seconds (without alignments) 2821.370 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued Patents NA:*
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    /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
    /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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4 US-09-643-990A-1
4 US-09-543-681A-2660
4 US-09-543-681A-2660
4 US-09-521-0178-971
4 US-09-221-0178-31
4 US-09-187-110
4 US-09-187-110
4 US-09-187-110
4 US-09-188-452A-1
4 US-09-188-452A-1
4 US-09-188-452A-1
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4 US-09-543-881A-2595
4 US-09-543-881A-2595
4 US-09-543-9130-751-389-3
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                                                                                                                                                                                                                                                                                        1 cagtecacaaataaacaaaetgtee 25
                                                                                                                                                                                                                                      US-09-963-285-1_COPY_378_402
25
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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70.4 1056 4
70.4 1056 4
70.4 148857 4
70.4 148857 4
70.4 148857 4
69.6 2411 4
69.6 2411 4
69.8 2559 4
68.8 1230025 4
68.8 1230025 4
68.0 56.4 4223 3
66.4 4223 4
66.4 4223 4
66.4 4223 4
66.4 5220 4
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Match Length DB
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65.6
65.6
65.6
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Perfect score:
                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                              OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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                                                                                                                                                            Run on:
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Gaps

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ZIP: 9404-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
OPERATE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 195
LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 17.6; DE; Pred. No. 76; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                  Score 17.6; DE Pred. No. 65; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 CAATCCACAGAGAACAAACTCTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 cagriccagararaaacacacreac 229
                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAGTCCACAATAAACAAACTGTC 24
                                                                                                                                                                                                                                                                                                                                     70.4%;
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Best Local Similarity 83.3%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Proteus mirabilis
US-09-543-681A-2690
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 83.3
Matches 20; Conservative
                                                                                                                                                                                   TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                     Query Match
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US-09-313-294A-195
US-09-313-294A-195
Sequence 195-Application US/09313294A
PETENT NO. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ico, Laura Y.
APPLICANT: Sherman, Bradley K.
ITILE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
                                                                                                                                                                                                                                                                                       Hamilton O. Smith
J. Craig Venter
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
The Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 1830121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug_2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-06-11
ATTORNEY/ACBNT INFORMATION:
REGISTRATION NUMBER: 40,302
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: 9B186PICI
TELECOMMUNICATION: NUMBER: 9B186PICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.6%; Score 18.4; D
95.0%; Pred. No. 76;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
COMPUTER: 20550
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
COMPUTER: ASSTEM: MS DOS v6.22
SOPTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ropology: linear sequence DESCRIPTION: SEQ ID NO: 1: US-09-643-990A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1005260 CCACAATAAACAAACTTTC 1005279
                                    1005260 CCACAAATAAACAAACTIIC 1005279
                                                                                                                                                                                                                          APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 301-610-5790
TELEPAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
                                                                                                                                                            Sequence 1, Application US/09643990A; Patent No. 6528289; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 CCACAAATAAACAAACTGTC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                          RESULT 2
US-09-643-990A-1
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USCOLIA-2690
Sequence 2690, Application US/09543681A
Facent No. 6605709
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
FRIOR APPLICATION NUMBER: US 60/128,706
FRIOR APPLICATION NUMBER: US 60/128,706
FRIOR APPLICATION NUMBER: US 60/128,706
FRIOR APPLICATION NUMBER: US 60/128,706
FRIOR SEQ ID NOS: 8344
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| Sequence 91, Application US/09221017B
| Patent No. 6444799
| GENERAL INFORMATION:
| APPLICANT: ROSS, Bruce C. INTER OF INFORMATION:
| TITLE OF INFORMICES: 1120
| CORRESPONDENCE ADDRESS: 1120
| ADDRESSEE: WORLIGON & FOERSTER STREET: 755 PAGE MILL ROAD
| CITY: Palo Alto
| STRTE: CA STATE: CA SCONTRY: USA
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                                                                                                                      Length 281;
                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700548714H1
US-09-313-294A-195
                                                                                                                      DB 4;
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Sequence 110, Application US/09157177

Sequence 110, Application US/09157177

Parent No. 6090558

GENERAL INFORMATION:
APPLICANT: Butler, John M.
APPLICANT: Monforte, Joseph A.
APPLICANT: Monforte, Joseph A.
TITLE OF INVENTION: REPERAT MARKERS
TITLE OF INVENTION: REPERAT MARKERS
TITLE OF INVENTION: REPERAT MARKERS
CURRENT APPLICATION NUMBER: US/09/157,177

CURRENT PILING DATE: 1998-09-18

RARLIER APPLICATION NUMBER: 60/059,415

SARLIER PILING DATE: 1997-09-19

NUMBER OF SEQ ID NOS: 135

SOFTWARE: PATENTIN DATE: 2.0
                                                                                                                                                                                                                                        Sequence 3, Application US/10254869

Requence 3, Application US/10254869

Retent No. 6653117

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION NUMBER: US/10/254,869
CURRENT APPLICATION NUMBER: US/10/254,869
CURRENT FILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
IJBUTCH: 148567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 70.4%; Score 17.6; DB 4; Length 148567; Best Local Similarity 83.3%; Pred. No. 1.46+02; Matches 20; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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69.6%; Score 17.4; DB 3; Length 350;
Best Local Similarity 94.7%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 1; Indels
                         Indels
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87125 CATTACACAGATAAGAAACTGTC 87148
                                                                                                                             87125 CATTACACAGATAAAGAAACTGTC 87148
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                                                                           1 CAGTCCACAATAAACAAACTGTC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature; LCCATION: (1)...(148567); CTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-09-157-177-110/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-157-177-110
                                                                                                                                                                                                                                        US-10-254-869-3
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Reguence 3, Application US/09801876B

Reguence 3, Application US/09801876B

Reguence 3, Application US/09801876B

GRNERAL INFORMATION:
APPLICANT: VE, Jame et al
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REPERBNCE: CLOO1160
CURRENT APPLICATION NUMBER: US/09/801,876B

CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 70.4%; Score 17.6; D
Best Local Similarity 83.3%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27340-20021.00
                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA: PP166
FILING APPLICATION NUMBER: PP1646
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION NUMBER: PC7/AU98/01023
APPLICATION NUMBER: PC7/AU98/01023
ATTORNEY/AGENT: 10-DEC-1998
ATTORNEY/AGENT: IRPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHERICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1187 CAGTCCACAACAACAATAGTC 1210
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAGTCCACAAATAAACAAACTGTC 24
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) LOCATION: (1)...(14857)

; CTHER INFORMATION: n = A,T,C or G

US-09-801-8768-3
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REPERENCE/DOCKET NUMBER: 273
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 706141
INFORMATION FOR SEQ ID NO: 971:
SEQUENCE CHARACTERISTICS:
LENGTH: 3615 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: 1...3615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-221-017B-971
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70.4%; Score 17.6; DB 4; Length 148567;

Query Match

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Sequence 17, Application US/09319588C

| Sequence 17, Application US/09319588C
| Patent NO. 6509018
| GENERAL INFORMATION:
| APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE-INSERM
| APPLICANT: INSTITUT PASTEUR
| APPLICANT: INSTITUT PASTEUR
| APPLICANT: INSTITUT PASTEUR
| APPLICANT: SIMON Francois
| APPLICANT: SIMON Francoise
| APPLICANT: SARRE-SINOUSSI, Francoise
| APPLICANT: SARRE-SINOUSSI, Francoise
| APPLICANT: BARRE-SINOUSSI, Francoise
| APPLICANT: BARRE-SINOUSSI, Francoise
| TITLE OF INVENTION: NON-M NON-O HIV STRAINS, FRAGMENTS AND APPLICATION NUMBER: US/09/319,588C
| CURRENT FILING DATE: 1996-12-09
| NUMBER OF SEQ ID NOS: 98
| SOFTWARE: Patentin Ver: 2.1
| SEQ ID NO 17
| LENGTH: 2559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match

68.8%; Score 17.2; DB 4;

Best Local Similarity 86.4%; Pred. No. 1.3e+02;

Matches 19; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GICCACAAATAAACAAACIGIC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (2556)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)
US-09-319-588C-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-319-588C-1
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                                                                  Sequence 15, Application US/09446301A

Sequence 15, Application US/09446301A

Patent No. 650633

GENERAL INPORMATION:
APPLICANT: EL SOLH
TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE
TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED
TITLE OF INVENTION: COMPOUNDS

TITLE OF INVENTION: COMPOUNDS

TITLE OF INVENTION: COMPOUNDS

TITLE OF INVENTION: UNMBER: US/09/446,301A

CURRENT FILING DATE: 1999-112-20

NUMBER OF SEQ ID NOS: 51

SOFTWARE PATENTY

SEQ ID NO 15

LENGTH: 2411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: E1 Solh, Nevine
APPLICANT: E1 Solh, Nevine
APPLICANT: E1 Solh, Nevine
TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE
TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED
TITLE OF INVENTION: CORPOUNDS
TITLE OF INVENTION: 0.0495.0173.0000
TITLE DEPERENCE: 0.3495.0173.0000
CURRENT APPLICATION NUMBER: 0.6/099,932
CURRENT PILING DATE: 1998-06-19
EARLIER RELING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Pred. No. 1e+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 47, Application US/09099932 Patent No. 6570001
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; LOCATION: (700..2355, 2388..2411)
US-09-446-301A-15
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Best Local Similarity 94.7%;
Matches 18; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Staphylococcus sp
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; LOCATION: (2388)..(2411)
US-09-099-932-47
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NAME/KEY: CDS
LOCATION: (700)..(2355)
                                  RESULT 9
US-09-446-301A-15/c
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US-09-099-932-47/c
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Gaps

3; Indels

Length 2559;

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE-INSERM
APPLICANT: INSTITUT PASTEUR
APPLICANT: MAUCIERE, Philippe
APPLICANT: COUSSERT-AJAKA, Ibtissam
APPLICANT: GUASSERT-AJAKA, Ibtissam
APPLICANT: SARGOSTI, Sentob
APPLICANT: SARGOSTI, Sentob
APPLICANT: SARGOSTI, Sentob
APPLICANT: SARGOSTI, Sentob
APPLICANT: SARGOSTI, Sentob
APPLICANT: NON-M NON-O HIV STRAINS, FRAGMENTS AND APPLICATIONS:
FILE REPERENECE: 598USL2
CURRENT APPLICATION NUMBER: US/09/319,588C
CURRENT FILING DATE: 1999-08-27
PRIOR PRILING DATE: 1996-12-09
NUMBER OF SEQ ID NOS: 98
SEGFFWARE: PALEALIN Ver. 2.1
SEQ ID NO 1
LENGTH: 9183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Human immunodeficiency virus type 1
1247 Grecacaarrracaarcrere 1226
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                                                                                                                                     Sequence 1, Application US/09319588C
Patent No. 6509018
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RESULT 11

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NAME/KEY: misc feature
LOCATION: (270501)..(285000)
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (345001)..(450000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (445001)..(450000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (445001)..(450000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (445001)..(450000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (450001)..(450000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (450001)..(450000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (450001)..(450000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (450001)..(525000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (450001)..(525000)
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NAME/KEY: misc feature
LOCATION: (450001)..(525000)
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LOCATION: (450001)..(525000)
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LOCATION: (450001)..(525000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (520001)..(52000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (540001)..(52000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (540001)..(520001)..(52000)
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LOCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (57001)..(585000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (585001). (600000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c or g
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                           RESULT 13
US-09-198-452A-1
Sequence 1, Application US/09198452A
Patent No. 655294
GENERAL INFORMATION:
TAPLICANT: GIIIFfais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 123025
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OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: (-0 or g or
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OTHER INFORMATION: n=a or c or g
NAME/KEY: misc feature
LOCATION: (30001)..(45000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (45001)..(60000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (75001)..(90000)
OTHER INFORMATION: n=a or c or g
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANICIA: Chlamydia pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) _ (15000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc feature
LOCATION: (15001)...(30000)
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 476
LENGTH: 438
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Sequence 1109, Application US/09833381

Sequence 1109, Application US/09833381

SERENT NO. 6672186

TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs

TITLE PERERNORS: 5800-119

CURRENT PILING DATE: 2001-04-11

PRIOR PELING DATE: 2000-04-11

PRIOR PELING DATE: 2000-02-9

NUMBER OF SEQ ID NOS: 2050

SOFTWARE: FRAISEQ for Windows Version 3.0

SEQ ID NO 1109

LENGTH: 505
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Pred. No. 1.2e+02;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335 cadricteaaaraaceracrares 311
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; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1109
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0%;
Matches 20; Conservative
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Best Local Similarity 80.03
Matches 20; Conservative
                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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US-09-833-381-1109/c
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LOCATION: (675001)...(690000)
OTHER INPORMATION: n=a or or g or t
NAME/KEY: misoc feature
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NAME/KEY: misoc feature
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NAME/KEY: misoc feature
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LOCATION: (85501)..(87000)
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NAME/KEY: misc feature
LOCATION: (87001)..(88500)
OTHER INFORMATION: n=a or or g or t
NAME/KEY: misc feature
LOCATION: (86501)..(90000)
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LOCATION: (90001)...(915000)
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NAME/KEY: misc_feature
                                                           OTHER INFORMATION: n=a or c or g or t NAME/Ker; misc feature LOCATION: (64501). (66000) OTHER INFORMATION: n=a or c or g or t NAME/Ker; misc feature LOCATION: (66001). (65500) OTHER INFORMATION: n=a or c or g or t OTHER INFORMATION: n=a or c or g or t
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0; Gaps

Query Match 68.8%; Score 17.2; DB 4; Length 1230025; Best Local Similarity 86.4%; Pred. No. 2e+02; Matches 19; Conservative 0; Mismatches 3; Indels 0;

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4 TCCACAAATAAACAAACTGTCC 25

RESULT 14
US-09-540-236-476/c
; Sequence 476, Application US/09540236
; Patent No. 6673910
; GRNERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.

Sequence 1095, Ap Sequence 11869, Ap Sequence 118026, Sequence 317, App Sequence 31069, A Sequence 31669, A Sequence 3169, A Sequence 21692, A Sequence 228782, Sequence 228782, Sequence 229332, Sequence 259331, Sequence 259331, Sequence 259332, Sequence 3242, A Sequence 32601, A Sequence 32601, A Sequence 32601, A Sequence 32601, A Sequence 32601, A Sequence 32601, A Sequence 32601, A

Sequence 3, Appli Sequence 3, Appli Sequence 2767, Ap Sequence 2767, Ap Sequence 3094, Ap

Sequence 1055, Ap Sequence 81, Appl Sequence 3, Appli

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15 US-10-227-577-1494
15 US-10-292-798-1095
15 US-10-292-798-1369
15 US-10-292-798-1369
15 US-10-292-798-1369
15 US-10-292-798-1369
15 US-10-21-714A-337
15 US-10-221-714A-337
15 US-10-221-714A-337
15 US-10-221-714A-337
15 US-10-27-632-36169
15 US-10-027-632-36169
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15 US-10-027-632-36130
15 US-10-027-632-259331
15 US-10-27-632-259332
15 US-10-27-632-259332
16 US-10-27-632-259332
17 US-10-27-632-259332
18 US-10-21-245-261
19 US-10-311-455-507
19 US-09-966-880A-95
19 US-09-966-880A-95
19 US-09-966-880A-95
19 US-09-966-880A-95
19 US-09-966-880A-95
19 US-09-966-880A-95
19 US-09-968-880A-95
19 US-09-9801-876B-9
19 US-09-9801-876B-9
19 US-09-988-842A-2767
19 US-10-254-886-3
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Matches 25; Conservative
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LENGTH: 6021
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Sequence 1, Appli
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCONB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCONB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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15: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO0N_SPUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/USO0N_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/USO0N_NEW_PUB.seq:*
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8 1907 15 U3-10-027-612-286-1

2 455 10 U3-09-918-995-26403

2 50000 13 U3-10-063-763-4

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6 1850121 14 U3-10-282-1225-0

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6 1850121 15 U3-10-329-960-1

6 1850121 15 U3-10-329-960-1

8 8 9 U3-09-910-343-313

8 22183 9 U3-09-764-889-1494
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Copyright (c) 1993 - 2004 Compugen Ltd.
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1 cagtccacaaataaacaaartmtnn <sup>3</sup>
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RESULT 1
US-09-963-285-5
Sequence 5, Application US/09963285
Sequence 5, Application US/09963285
Sequence 5, Application US/09963285
Sequence 6, Application US/0963285
Sequence 7
GENERAL INFORMATION:
APPLICANT: Enerbock, Katarina APPLICANT: Rondahl, Lena APPLICANT: Rondahl, Lena APPLICANT: Rondahl, Lena APPLICANT: Wasserman, Wyeth TILLE OF INVENTION: PROMOTER SEQUENCES FILE REFERENCE: 13425-042001
CURRENT APPLICATION NUMBER: US/09/963, 285
CURRENT FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
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Gaps
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Best Local Similarity 87.5%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 286, Application US/10085117
| Sequence 286, Application US/10085117
| Publication No. US2003023234A1
| GENERAL INFORMATION:
| APPLICANT: Moris, David W. |
| APPLICANT: Moris, David W. |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER |
| TITLE OF INVENTION: NOVEL COMPOSITION AND METHODS FOR CANCER |
| TITLE OF INVENTION: NOVEL COMPOSITION AND METHODS FOR CANCER |
| TITLE OF INVENTION: NOVEL 202-27 |
| CURRENT APPLICATION NUMBER: US/10/085,117 |
| CURRENT APPLICATION NUMBER: US 09/798,586 |
| PRIOR APPLICATION NUMBER: US 09/798,586 |
| PRIOR ALPUR FILING DATE: 2002-03-02 |
| NUMBER OF SEQ ID NOS: 361 |
| SEQ ID NO 286 |
| LINGTHAN APPLICATION NUMBER: US/10 |
| SEQ ID NO 286 |
| LINGTHAN APPLICATION NUMBER: US/10 |
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                                                                                                                                                                           DB 15; Length 1907;
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PUBLICATION NO. US20330073623A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hyesq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: REAM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT PILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 1999-01-20
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: PSESEEQ for Windows Version 3.0
SEQ ID NO 26403
LENGTH: 455
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                       Query Match

80.8%; Score 20.2; Dest Local Similarity

88.0%; Pred. No. 62;
Matches

22; Conservative

0; Mismatches
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CCATION: (1)...(455)
OTHER INFORMATION: n = A,T,C or G
US-09-918-955-26403
; LOCATION: (1)...(1907)
; CTHER INFORMATION: n = A,T,C or G
US-10-027-632-53050
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Best Local Similarity 90.99
Matches 20; Conservative
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CRGANISM: Homo sapiens
US-10-085-117-286
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US-09-918-995-26403
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; Bublication No. US20030204075A9
; Publication No. US20030204075A9
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE REFERENCE: 108927.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR PELICATION NUMBER: US 60/18,006
; PRIOR PELICATION NUMBER: US 60/18,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-09-28
; PRIOR FILING DATE: 1999-09-09
; PRIOR FILING DATE: 1999-08-09
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Best Local Similarity 100.0%; Score 25; DB 9; Length 6458;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                          US-09-963-285.
US-09-963-285.
Sequence 1, Application US/09963285
Patent No. US2002009707A1
GENERAL INFORMATION:
APPLICANT: Enerbck, Sven
APPLICANT: Krook, Katarina
APPLICANT: Rondahl, Lena
APPLICANT: Rondahl, Lena
APPLICANT: Wasserman, Wyeth
TITLE OF INVENTION: PROWOTER SEQUENCES
FILE REFREENT APPLICATION NUMBER: US/09/963, 285
CURRENT APPLICATION NUMBER: SE 0004102-0
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR APPLICATION NUMBER: SE 0003435-5
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 1
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; LOCATION: (2235)...(3737)
US-09-963-285-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM; Human
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US-10-027-632-53050
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TITLE OF INVENTION: No. US20030022286Alel Transporter-Like Genes and Uses Therefor FILE REFERENCE: 10147-8
CURRENT APPLICATION NUMBER: US/10/060,763
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 50000
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Sequence 2550, Application US/10027632

Publication No. US2030204075A9

GENERAL INFORMATION:

APPLICANT Warg David G.

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR PILING DATE: 2002-04-30

PRIOR PILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR PLING DATE: 1090-04-20

PRIOR PLING DATE: 1090-04-20

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR PRIOR PILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PRIOR PILING DATE: 1999-10-26

PRIOR PILING DATE: 1999-10-26

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

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PRIOR PILING DATE: 1999-08-08

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Pred. No. 4.6e+02;
0; Mismatches 2;
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
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Best Local Similarity 90.9%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-763-4
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US-10-282-122A-22176/c
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ORGANISM: Human
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US-10-027-632-2550
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US-310-063-763-4/c

Sequence 4, Application US/10063763

Sequence 10 No. US20010001663A1

SEQUENCE 10 NO. US20010001663A1

APPLICANT: Curtis, Rory A.J.

ITILE OF INVENTION:

PILE REPRENCE: 10147-8

CURRENT APPLICATION NUMBER: US/10/063,763

CURRENT FILING DATE: 2002-01-30

PRIOR FILING DATE: 1999-JUL-30

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 4

SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 464;
                                                                                                                                                                                                                                                                                               APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT RILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER: OF SEQ ID NOS: 38054
SOFTWARE: FSESSEQ for Windows Version 3.0
SEQ ID NO 2704
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                                                                                                                                                                                                          Sequence 27704, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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                             376 TACACAAAAAACAAACTGTCC 397
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US-09-918-995-27704
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Best Local Similarity 90.9
Matches 20; Conservative
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CORGANISM: Homo sapiens
US-10-063-763-4
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: (1)...(464)
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US-10-060-763-4/c
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NAME/KEY: misc feature
LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals a, t, g or c
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NAME/KEY: misc_feature
LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals a, t,
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LOCATION: (44905)..(44905)
OTHER INFORMATION: n equals a,
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LOCATION: (44416)..(44416)
OTHER INFORMATION: n equals a,
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LOCATION: (44975)..(44975)
DTHER INFORMATION: n equals a,
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LOCATION: (45732)..(45732)
OTHER INFORMATION: n equals a,
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LOCATION: (47036)..(47036)
THER INFORMATION: n equals a,
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LOCATION: (51602)...(51602)
JTHER INFORMATION: n equals a,
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OCATION: (45593)..(45593)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals a,
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LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (4747)...(4747)
JTHER INFORMATION: n equals a,
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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals a,
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LOCATION: (51786)..(51786)
JTHER INFORMATION: n equals
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LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (36543)..(36543)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (9921)
OTHER INFORMATION: n equals
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LOCATION: (51334)..(51
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US-10-329-960-1
Sequence 1, Application US/10329960
| Publication No. US2030099277A1
| GENERAL INFORMATION:
| APPLICANT: Fleischmann et al. |
| TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag TITLE OF INVENTION: NUMBER: US/10/329,960
| TITLE OF INVENTION: Thereof, and Uses Thereof
| FILE REFERENCE: PB186P1
| CURRENT PILING DATE: 2003-01-02
| PRIOR PILING DATE: 1995-06-07
| PRIOR FILING DATE: 1995-04-21
| PRIOR FILING DATE: 1995-04-21
| RING APPLICATION NUMBER: US 08/426,787
| PRIOR FILING DATE: 1995-04-21
| NUMBER OF SEQ ID NOS: 1
| SEQ ID NO 1
| LENGTH: 1830121
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TITLE OF INVENION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: BLITRA.034A
CURRENT APPLICATION NUMBER: 05/10/202,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
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ORGANISM: Haemophilus influenzae
FBATURE:
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CRGANISM: Haemophilus influenzae
US-10-282-122A-22176
          Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 95.0
Matches 19; Conservative
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NAME/KEY: misc feature
LOCATION: (139910)..(139910)
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OCATION: (102696)..(102696)
THER INFORMATION: n equals a, t, g
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OCATION: (105121)..(105121)
THER INFORMATION: n equals a, t, 9
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OCATION: (119750)..(119750)
THER INFORMATION: n equals a, t,
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ACATION: (120038)..(120038)
THER INFORMATION: n equals a,
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OCATION: (122336)..(122336)
THER INFORMATION: n equals a,
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LOCATION: (117136)..(117136)
THER INFORMATION: n equals a,
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OCATION: (122167)..(122167)
THER INFORMATION: n equals a,
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OCATION: (131340)..(131340)
YTHER INFORMATION: n equals a,
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FION: (119924)
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OCATION: (121344)...(121344)
THER INFORMATION: n equals a,
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LCCATION: (65309)..(65309)
OTHER INFORMATION: n equals a,
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LOCATION: (65313)..(65313)
UTHER INFORMATION: n equals a,
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OCATION: (80024). (80024)
OTHER INFORMATION: n equals a,
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OCATION: (100091)..(100091)
THER INFORMATION: n equals a,
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OCATION: (107248)..(107248)
THER INFORMATION: n equals a,
LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals a,
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LOCATION: (140398)..(140398)
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LOCATION: (131360)..(131360)
DTHER INFORMATION: n equals
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US-10-329-6/U-1

| Sequence II Application US/10329670
| Publication No. US20040018503A1
| GENERAL INFORMATION:
| APPLICANTY: Fleisofolmann et al. |
| TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fragrittle OF INVENTION: Thereof, and Uses Thereof |
| TITLE OF INVENTION: Thereof, and Uses Thereof |
| TITLE OF INVENTION: Thereof, and Uses Thereof |
| TITLE OF INVENTION: Thereof, and Uses Thereof |
| TITLE OF INVENTION: Thereof, and Uses Thereof |
| TITLE OF INVENTION: Thereof, and Uses Thereof |
| TITLE OF INVENTION: Thereof, and Uses Thereof |
| CURRENT FILING DATE: 2002-12-24 |
| PRIOR FILING DATE: 1995-06-07 |
| PRIOR PAPLICATION NUMBER: US 08/426,787 |
| PRIOR PAPLICATION NUMBER: US 08/426,787 |
| PRIOR PAPLICATION NUMBER: US 08/426,787 |
| PRIOR PAPLICATION NUMBER: US 08/426,787 |
| PRIOR PAPLICATION NUMBER: US 08/426,787 |
| PRIOR PAPLING DATE: 1995-04-21 |
| NUMBER OF SEQ ID NOS: 1 |
| SEQ ID NO 1 |
| LENGTH: 1830121 |
| WARREN OF SEQ ID NO 1 |
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LOCATION: (9921)..(9921)
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NAME/KEY: misc_feature
LOCATION: (152500). (152500)
OTHER INFORMATION: n equals a, t, g or FEATURE:
NAME/KEY: misc_feature
LOCATION: (152530). (152530)
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ORGANISM: Haemophilus influenzae
FEATURE:
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LOCATION: (4747)...(4747)
OTHER INFORMATION: n equals a,
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NAMB/KEY: misc_feature
LOCATION: (145942). (145942)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc feature
LOCATION: (147197)...(147197)
OTHER INFORMATION: n equals a,
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LOCATION: (150841)...(150841)
OTHER INFORMATION: n equals a,
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NAME/KEX: misc_feature
LOCATION: (145171)..(145171)
OTHER INFORMATION: n equals a,
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LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc feature
LOCATION: (145058) ..(145058)
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US-10-329-670-1
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NAME/KEY: misc feature
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COCATION: (65309)..(65309)
OTHER INFORMATION: n equals a, t,
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LOCATION: (44975)..(44975)
THER INFORMATION: n equals a, t,
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LOCATION: (47036)..(47036)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc feature
LOCATION: (29298)..(29298)
CTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (36543). (36543)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals a,
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NAME/KEX: misc_feature
LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals a,
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LOCATION: (44905)...(44905)
OTHER INFORMATION: n equals a,
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LOCATION: (45732)..(45732)
OTHER INFORMATION: n equals a,
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LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals a,
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LOCATION: (51786)..(51786)
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NAME/KEY: misc feature
LOCATION: (10150)..(10150)
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LOCATION: (36636)..(36636)
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LOCATION: (44416)..(44416)
DTHER INFORMATION: n equals a,
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LOCATION: (36551)..(36551)
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals a, t, g or
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LOCATION: (120038)...(120038)
COTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (122167)...(122167)
LOCATION: (122167)...(122167)
OTHER INFORMATION: n equals a, t,
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LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals a,
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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NAME/KRY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc feature
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publication No. US20030059908A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFRENCE: PC007C1

CURRENT FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 2442

Prior Application removed - See File Wrapper or Palm

SOFTWARE: Patentin Ver. 2.0

FEQ ID NO 1494
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Frior application data removed - refer to PALM or file wrapper NUMBER: OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1494
LENGTH: 32183
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72.8%; Score 18.2; DB 9;
Best Local Similarity 87.0%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 3;
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; ORGANISM: Homo sapiens
US-10-091-504-1494
                                                                                                                                                                                                                TYPE: DNA
CNGANISM: Homo sapiens
US-09-764-869-1494
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US-10-091-504-1494/c
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Sequence 313, Application US/09910943
Patent No. US20020081610A1
GENERAL INFORMATION:
APPLICANT: Hermati-Erivanlou, Ali
APPLICANT: Altuman, Curtis
TILLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
TILLE OF INVENTION WIMBER: US/09/910,943
CURRENT APPLICATION WIMBER: 2001-07-23
NUMBER OF SEQ ID NOS: 742
SOFTWARE PATENTIN Version 3.1
SEQ ID NO 313
LENGTH: 686
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73.6%; Score 18.4; DB 15; Length 1830121;
Best Local Similarity 95.0%; Pred. No. 9.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; G
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; LOCATION: (1)._(686)
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NAME/KEX: misc feature
LOCATION: (152500)
OTHER INFORMATION: n equals a,
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LOCATION: (145171)...(145171)
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NAME/KEY: misc feature
LOCATION: (147197)
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LOCATION: (145942) .. (145942)
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LOCATION: (152530)..(152530)
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US-09-910-943-313/c
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Gaps

Length 686;

Query Match 72.8%; Score 18.2; DB 9; Length 6 Best Local Similarity 87.0%; Pred. No. 3.7e+02; Matches 20; Conservative 0; Mismatches 3; Indels

345 cagriccacaaargaccaaacggr 323

ò g Sequence 1494, Application US/09764869; Patent No. US20020061521A1 GENERAL INFORMATION: APPLICANT: Rosen et al.

US-09-764-869-1494/c

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March 25, 2004, .08:39:03 , Search time 170.338 Seconds (without alignments) 6361.316 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                   3470272 seqs, 21671516995 residues
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	08222 M.muscul	1108 Ношо зар	Mus mu	Mus mus	Mouse	Danio re	Danio r	Rattus	Sequen	Trypan	HOMO B	nan ol	HOMO B	JIYZA HOHO B	Orvza	AC114142 Rattus no	Rattus	Mus	Mus	Homo	Homo	Ношо	Homo	ACO12336 NOWO SAPI ACO46156 Homo sapi	Ношо	Homo	Mus	Ношо	Human Homo e	Mus mu	Ношо	Mus	AC112156 Mus muscu AC000460 Homo sapi	Ношо	Humar	Ношо	AC125080 Mus muscu		700 - VEM. 14-MAY-1997	7		ene.	Vertebrata; Euteleostomi; thi; Muridae; Murinae; Mus.	and Sugiyama, T.	FKHL 14) mesenchyme gene and protein
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•	Query Ce Match Length DB	5 100 0 6021	5 100.0 168	5 100.0 178416	4 RS 6 162337	8 83.2 202972	4 81.6 166829	2 80.8 178491	2 80.8 222745	8 79.2 1019	2.67 2.693	26638 79.7 86992	8 79.2 100849	8 79.2 113200	8 79.2 139503	8 79.2 163543	8 79.2 187234	8 79.2 218347	4 79.2 297898	4 77.6 209907	.2 76.8 70313	.2 76.8 101281	2 76.8 104017	.2 76.8 107430	.2 76.8 112527 2 76.8 132775	.2 76.8 137924	.2 76.8 142959	.2 /6.8 144264 2 76 0 150310	.2 76.8 164376	.2 76.8 164550	.2 76.8 1646U3	.2 76.8 169883	.2 76.8 173829	.2 76.8 175208 1	7,551 1,574 5 7,5 8 175749	2 76.8 175988	.2 76.8 176267	.2 76.8 181087			MFH-1	O,	mesenchyme fork head Mus musculus (house	Mus musculus Eukaryota; Metazoa; Mammalia; Eutheria;	1 Miura, N., Iida, K.,	Isolation of the mouse head-1 genes reveals co
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Drive, Walnut Creek, CA 94598, USA
On Oct 29, 2002 this sequence version replaced gi:13786306.
Draft Sequence Produced by DOB Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                           1. 168656
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Unpublished (2001)
3 (bases 1 to 178416)
McPherson, J.D. and Waterston, R.H.
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Submitted (06-AUG-2003)
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Wilson, R.
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Best Local Similarity 100.
Matches 25; Conservative
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ORGANISM
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AC127554
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Direct Submission
Direct Submission
Submitted (18-SEP-1996) N. Miura, Akita University School of
Submitted, Department of Biochemistry, 1-1-1 Hondo, Akita 010, JAPAN
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            Codon start=1
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 168556)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryoffa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 168656)

DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission
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Submitted (29-OCT-2002) DOB Joint Genome Institute, 2800 Mitchell
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Homo sapiens chromosome 16 clone RP11-46309, complete sequence.
AC009108
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DOE Joint Genome Institute.
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Best Local Similarity 100.
Matches 25; Conservative
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Direct Submission
Submitted (27-NOV-2003) Department of Genetics, Washington
Submitted (27-NOV-2003) Department of Genetics, Wissouri 63108, USA
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Aug 6, 2003 this sequence version replaced gi:33342444.
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Mus musculus BAC clone RP24-323K23 from chromosome 8, complete
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4 (bases 1 to 178416)
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Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 178416)
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www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
Finishing Completed at Stanford Human Genome Center and Los Alamos
Mational Laboratory
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Bstimated Total Number of Errors is 0.2.
Location/Qualifiers
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Cordes, M. and Haglund, K.
The sequence of Mus musculus BAC clone RP24-323K23
Unpublished (2001)
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Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
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rpt_family="Alu"
1423. :52857
1423. :52857
3367. :52484
13. :52484
4128. :54233
4128. :54233
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5873. .35982
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25838 . 26022
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2257 . 27380
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28700 . 28893
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0859. .30
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0809.
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                                                                                                                                                                                                                                                                                                                                                                               The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                               this
                                                                                                                                                         all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                              NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone is
overlapped by AC124170.
                                                                                                                                             This sequence was finished as follows unless otherwise noted:
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/note="CpG island (%GC=69.2, o/e=0.78, #CpGs=269)"
[648. .16980
'rpt, family="MIR"
8383. .1840^4
   Center project name: M BB0323K23
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'organism="Mus musculus"
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/chromosome="8"
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clone_lib="RPCI-24"
791. .1839
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19821. .20013
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20188. .20538
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3834. 3845
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3846. 3972
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973. .4026
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